

Result No.	Score	Query Match	Length	DB	ID	Description	
1	39	1.0	38703	7	US-11-052-544-28	Sequence 28, Appl	
2	33	0.8	3268	1	US-10-793-626-3394	Sequence 3394, Ap	
3	32.2	0.8	1748	1	US-10-689-742-67	Sequence 67, Appl	
4	32.2	0.8	2175	1	US-10-821-234-654	Sequence 654, App	
C 5	32.2	0.8	7240	1	US-10-496-711-25	Sequence 25, Appl	
6	31.6	0.8	13672	7	US-11-055-035-2	Sequence 2, Appl	
7	31.4	0.8	23459	1	US-10-962-756A-1	Sequence 1, Appl	
8	31.2	0.8	2956	1	US-10-689-742-103	Sequence 103, Appl	
C 9	31	0.8	340000	7	US-11-102-978-3	Sequence 3, Appl	
10	30.4	0.8	2031	7	US-11-135-855-5	Sequence 5, Appl	
11	30.4	0.8	2154	7	US-11-135-855-6	Sequence 6, Appl	
12	30.4	0.8	2596	8	US-11-112-944-1	Sequence 1, Appl	
13	30.4	0.8	7980	1	US-10-509-921-4	Sequence 4, Appl	
14	30.4	0.8	7980	1	US-10-509-921-5	Sequence 5, Appl	
15	30.4	0.8	7983	1	US-10-509-921-7	Sequence 7, Appl	
16	30.4	0.8	340000	7	US-11-102-978-3	Sequence 3, Appl	
C 17	30.2	0.8	609	1	US-10-793-626-2363	Sequence 2363, Ap	
18	30.2	0.8	3246	1	US-10-793-626-3459	Sequence 3459, Ap	
19	30	0.8	888	1	US-10-821-234-739	Sequence 739, Appl	
20	30	0.8	3221	1	US-10-793-626-4163	Sequence 4163, Ap	
21	30	0.8	3423	1	US-10-793-626-3355	Sequence 3355, Ap	
22	30	0.8	4557	9	US-11-060-920-3	Sequence 3, Appl	
C 23	29.8	0.8	9930	1	US-10-793-626-355	Sequence 355, Appl	

```
US-10-793-626-3394
; Sequence 3394, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3394
; LENGTH: 3268
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-10-793-626-3394

Query Match          0.8%; Score 33; DB 1; Length 3268;
Best Local Similarity 53.3%; Pred. No. 7.8;
Matches 69; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 2563 AAATTACTTCTTCTTGCAATGACTAAACGGCTTCCATTCTTGATCCATTTTAGAGAC 2622
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2892 AAAACACTTCTATTATTATTAATACAAACATGATTACCAATTAACTTATATAAGTT 2951
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2623 GAACCTTAATCGGTGCTTATCTCGAAGCGGTGGTTCCTCGATCTTGCTTGTCTTCC 2682
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2952 GAACGCTTTAAGGAGGATATTTCTTCTTAAAGCGTTCTTCAGTATTCGTTTAAATTTT 3011
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2683 AAATACAAT 2691
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 3012 AACTAGAAAT 3020
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 3
US-10-689-742-67
; Sequence 67, Application US/10689742
; Publication No. US20050250180A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M
; APPLICANT: LaVallie, Edward R
; APPLICANT: Racie, Lisa A
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Spaulding, Vikki
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: 00766.000091.10
; CURRENT APPLICATION NUMBER: US/10/689,742
; CURRENT FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: 09/746,793
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 67
; LENGTH: 1748
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-689-742-67

Query Match          0.8%; Score 32.2; DB 1; Length 1748;
Best Local Similarity 46.9%; Pred. No. 8.8;
Matches 100; Conservative 0; Mismatches 113; Indels 0; Gaps 0;

QY 2393 AAGCACTAATAGAGTCTTTATGTTCTGTTTGTATGAGACTTCTTCGACAGCTTCGAC 2452
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 945 AAGAGCTACTCGATCAGTTGAGCTTGCTGTAGTGGGATGTCGTGAGTGGAGTGATGATC 1004
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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QY 2453 ATGGATGTTTCACCGACTCTCTCAGAGACAAAGCCGTTCCAGGATAAACTTCGAGAGAAAT 2512
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1005 AAGCTGTATTACCTTTTGTATTATGACACGATACAACTCACCATCACCTTTTGAAGAGTCAG 1064
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2513 TTGTCAGATCGACACGATATGCTTACGCTGTGAGGATGTTTTTGATGCTAAATTAATTC 2572
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1065 TTGTTGGTTTCCCTTCTCTGGACAAGCGTTATAGGAAGATTGTTGATGTCAATTTTCAAT 1124
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2573 TTCTTGCAATGACTAAACCGCTTCCATTCT 2605
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1125 CTCGTGTAGATGAGGATCAAGCTCTCTCTCT 1157
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 4
US-10-821-234-654
; Sequence 654, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 654
; LENGTH: 2175
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-821-234-654

Query Match          0.8%; Score 32.2; DB 1; Length 2175;
Best Local Similarity 51.0%; Pred. No. 10;
Matches 76; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

QY 1374 CCAATTTTCTTAGAAAAAGGTATGGAACCTTTCGACAGATGATGGAGGATCGGCTGAG 1433
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 634 CCCATCACCTTTTATTGGAGAAGGAACGAGAGAAGAAATTTAGTGATGATGAGGCAGAG 693
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1434 AAGGATATGCGCTGGGAGAGTCCGCCGTGAAAAAGAGCAACCACTCCGAGACCGAA 1493
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 694 GAAGAGAAAGGTGAGAAAGAGAGAGGAGAGATTAAGATGATGAAGAAAGCCCAAGATCGAA 753
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1494 GGAGTCGATGTAAAGGATTGGGTGCTGAG 1522
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 754 GATGTCGGTTCAGATGAGGAGGATGACAG 782
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 5
US-10-496-711-25/c
; Sequence 25, Application US/10496711
; Publication No. US20050256649A1
; GENERAL INFORMATION:
; APPLICANT: SmithKline Beecham Corporation
; TITLE OF INVENTION: HIGH THROUGHPUT CORRELATION OF
; TITLE OF INVENTION: POLYMORPHIC FORMS WITH MULTIPLE PHENOTYPES WITHIN CLINICAL
; TITLE OF INVENTION: POPULATIONS
; FILE REFERENCE: PU4699WO
; CURRENT APPLICATION NUMBER: US/10/496,711
; CURRENT FILING DATE: 2004-05-26
; PRIOR APPLICATION NUMBER: 60/344892
; PRIOR FILING DATE: 2002-12-21
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 7240
; TYPE: DNA
```

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; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 23459
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1804)..(1804)
; OTHER INFORMATION: n is the reference allele 'g' which can also be the variant
; OTHER INFORMATION: allele 'a'
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (8872)..(8872)
; OTHER INFORMATION: n is the reference allele 't' which can also be the variant
; OTHER INFORMATION: allele 'c'
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (9166)..(9166)
; OTHER INFORMATION: n is the reference allele 'c' which can also be the variant
; OTHER INFORMATION: allele 't'
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (12699)..(12699)
; OTHER INFORMATION: n is the reference allele 'g' which can also be the variant
; OTHER INFORMATION: allele 'a'
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (17145)..(17145)
; OTHER INFORMATION: n is the reference allele 'c' which can also be the variant
; OTHER INFORMATION: allele 't'
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (17258)..(17258)
; OTHER INFORMATION: n is the reference allele 'g' which can also be the variant
; OTHER INFORMATION: allele 'a'
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (19819)..(19819)
; OTHER INFORMATION: n is the reference allele 'c' which can also be the variant
; OTHER INFORMATION: allele 't'
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (19833)..(19833)
; OTHER INFORMATION: n is the reference allele 't' which can also be the variant
; OTHER INFORMATION: allele 'c'
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (19943)..(19943)
; OTHER INFORMATION: n is the reference allele 'c' which can also be the variant
; OTHER INFORMATION: allele 't'
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (19971)..(19971)
; OTHER INFORMATION: n is the reference allele 'g' which can also be the variant
; OTHER INFORMATION: allele 't'
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (20020)..(20020)
; OTHER INFORMATION: n is the reference allele 'c' which can also be the variant
; OTHER INFORMATION: allele 't'
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (20800)..(20800)
; OTHER INFORMATION: n is the reference allele 't' which can also be the variant
; OTHER INFORMATION: allele 'c'
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (20800)..(20800)
; OTHER INFORMATION: n is the reference allele 't' which can also be the variant
; OTHER INFORMATION: allele 'c'
; US-10-962-756A-1
;
Query Match          0.8%; Score 31.4; DB 1; Length 23459;
Best Local Similarity 51.0%; Pred. NO. 1.1e+02;
Matches 74; Conservative 0; Mismatches 71; Indels 0; Gaps 0;
Qy 3808 TCTACGTGCTATCGCTCGGACTCTCTTCTTACCCCTATATATTCCATCGTC 3867
||||| ||| | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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Db 4039 TCTATCTCGCTTTCTGTAGCTCTCTCTCTTATCTCTGTCTCCCTCCCTTATCTGTC 4098  
QY 3868 TGTATATTGTCATACGACGTCCTGTGTCGTCACATCAATATTCAGCCTCTTTCATGCTT 3927  
Db 4099 TTCCCTTTTGCCTGTCACTATCTCTGACCTCTTCTCTGTCACTTCTCTTTTCAGTGTCT 4158  
QY 3928 CTGTGTCCTCATAGATGTCATCTTC 3952  
Db 4159 CTGTTTCACTCTCTCTTTGTTTC 4183

RESULT 8  
US-10-689-742-103  
; Sequence 103, Application US/10689742  
; Publication No. US20050250180A1  
; GENERAL INFORMATION:  
; APPLICANT: Jacobs, Kenneth  
; APPLICANT: McCoy, John M  
; APPLICANT: Lavalie, Edward R  
; APPLICANT: Racie, Lisa A  
; APPLICANT: Evans, Cheryl  
; APPLICANT: Merberg, David  
; APPLICANT: Treacy, Maurice  
; APPLICANT: Spaulding, Vikki  
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM  
; FILE REFERENCE: 00766.000091.10  
; CURRENT APPLICATION NUMBER: US/10/689,742  
; PRIOR FILING DATE: 2003-10-22  
; PRIOR APPLICATION NUMBER: 09/746,783  
; PRIOR FILING DATE: 2000-12-21  
; NUMBER OF SEQ ID NOS: 231  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 103  
; LENGTH: 2956  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-689-742-103

Query Match 0.8%; Score 31.2; DB 1; Length 2956;  
Best Local Similarity 58.7%; Pred. No. 27;  
Matches 54; Conservative 0; Mismatches 38; Indels 0; Gaps 0;  
QY 2684 AATCAATACGGATTATTGCTCATCTGATTGGTCTACGGGCTGTGGAAATTTAACTAGT 2743  
Db 1207 AATGATTTTGTAGTTATTTTCTTAATGATACCGAGTCACCTTCGGGGCTAACTAAACATT 1266  
QY 2744 TTGTTAAGGAGTCTCTTCGCTAGACCCCTCT 2775  
Db 1267 TTGTGAGCATCTCTTAGTTTACATCCTCT 1298

RESULT 9  
US-11-102-978-3/c  
; Sequence 3, Application US/11102978  
; Publication No. US20050250142A1  
; GENERAL INFORMATION:  
; APPLICANT: University of Utah Technology Transfer Office  
; APPLICANT: University of Utah Research Foundation  
; TITLE OF INVENTION: Diagnosis and Treatment of Herpes Simplex Virus Disease  
; FILE REFERENCE: 0274-5537.1US  
; CURRENT APPLICATION NUMBER: US/11/102,978  
; CURRENT FILING DATE: 2005-04-11  
; PRIOR APPLICATION NUMBER: PCT/US2003/033152  
; PRIOR FILING DATE: 2003-10-18  
; PRIOR APPLICATION NUMBER: 60/419,576  
; PRIOR FILING DATE: 2002-10-18  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 3  
; LENGTH: 340000  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:

; NAME/KEY: exon  
; LOCATION: (56948)..(57115)  
; OTHER INFORMATION: C2lorf34 exon  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (80006)..(81089)  
; OTHER INFORMATION: Gene VDACC2P; voltage-dependent anion channel isoform 2 pseudogene  
; FEATURE:  
; NAME/KEY: exon  
; LOCATION: (167308)..(167438)  
; OTHER INFORMATION: C2lorf34 exon  
; FEATURE:  
; NAME/KEY: exon  
; LOCATION: (216732)..(216833)  
; OTHER INFORMATION: C2lorf34 exon  
US-11-102-978-3

Query Match 0.8%; Score 31; DB 7; Length 340000;  
Best Local Similarity 55.0%; Pred. No. 4.1e+02;  
Matches 61; Conservative 0; Mismatches 50; Indels 0; Gaps 0;  
QY 3832 GACTCTCTTTACCCCTATATATTATTCATCCGCTCTGTATATTTGTCTATCAGCAGTC 3891  
Db 81435 GGCATCTTTGTCTTCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATC 81376  
QY 3892 TGTGTCGTCACACTCAATATTCAGCCCTCTTCATGCTTCTGTGTCCTCATAGA 3942  
Db 81375 TACCTACCTATCTACTGCTATCTATCTTACTGATTCTGTTCTTAAGCAGA 81325

RESULT 10  
US-11-135-855-5  
; Sequence 5, Application US/11135855  
; Publication No. US20050255557A1  
; GENERAL INFORMATION:  
; APPLICANT: SMITHKLINE BEECHAM CORPORATION  
; APPLICANT: SMITHKLINE BEECHAM P.L.C.  
; TITLE OF INVENTION: NOVEL COMPOUNDS  
; FILE REFERENCE: GP50013  
; CURRENT APPLICATION NUMBER: US/11/135,855  
; CURRENT FILING DATE: 2005-05-24  
; PRIOR APPLICATION NUMBER: US/10/203,708  
; PRIOR FILING DATE: 2002-08-13  
; PRIOR APPLICATION NUMBER: PCT/US01/04703  
; PRIOR FILING DATE: 2001-02-14  
; PRIOR APPLICATION NUMBER: 60/182,172  
; PRIOR FILING DATE: 2000-02-14  
; PRIOR APPLICATION NUMBER: 60/186,084  
; PRIOR FILING DATE: 2000-02-29  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 5  
; LENGTH: 2031  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-135-855-5

Query Match 0.8%; Score 30.4; DB 7; Length 2031;  
Best Local Similarity 61.2%; Pred. No. 37;  
Matches 49; Conservative 0; Mismatches 31; Indels 0; Gaps 0;  
QY 1395 ATGGAACCTTGTGCACAAGATGATGGAGGATCGGCTGAGAAGGATATGCCCTGGGAGAG 1454  
Db 1663 ATCGAGCGGTGCAGAAAGTGACAAAGGCTGGATGAGAGAGAGAGCCGAGAGAG 1722  
QY 1455 TCGGCGGTGAAAAAGAGGC 1474  
Db 1723 CTGGCGGGGAGGAGCTGCG 1742

RESULT 11  
US-11-135-855-6  
; Sequence 6, Application US/11135855



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; Publication No. US20050250093A1
; GENERAL INFORMATION:
; APPLICANT: SmithKline Beecham Corporation
; TITLE OF INVENTION: Hepatitis C Virus Sub-Genomic Replicons
; FILE REFERENCE: P51335
; CURRENT APPLICATION NUMBER: US/10/509,921
; CURRENT FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: 60/369,685
; PRIOR FILING DATE: 2002-04-03
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 7980
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The polynucleotide sequence encodes sequences from
; US-10-509-921-4

. Query Match 0.8%; Score 30.4; DB 1; Length 7980;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
Matches 64; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

Qy 369 CCGAGGCCGGAACGAGACAGACACACCATCATCATCAGCCATGTCTTTTGTGATCGTTT 428
Db 7752 CCGATGAAGGTTGGGGTAAACATCCGGCCTCTTAAGCCATTCCTGTTTTTTTTTTT 7811

Qy 429 TTACATACTACCCGTCGATTCTAACTTCTTTCTTCTCTTGCCATCTTGCATTCTC 488
Db 7812 TTTTCTTTTCTTTTCTTTTCTTTTCTTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 7871

RESULT 14
US-10-509-921-5
; Sequence 5, Application US/10509921
; Publication No. US20050250093A1
; GENERAL INFORMATION:
; APPLICANT: SmithKline Beecham Corporation
; TITLE OF INVENTION: Hepatitis C Virus Sub-Genomic Replicons
; FILE REFERENCE: P51335
; CURRENT APPLICATION NUMBER: US/10/509,921
; CURRENT FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: 60/369,685
; PRIOR FILING DATE: 2002-04-03
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 7980
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The polynucleotide sequence encodes sequences from
; US-10-509-921-5

. Query Match 0.8%; Score 30.4; DB 1; Length 7980;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
Matches 64; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

Qy 369 CCGAGGCCGGAACGAGACAGACACACCATCATCATCAGCCATGTCTTTTGTGATCGTTT 428
Db 7752 CCGATGAAGGTTGGGGTAAACATCCGGCCTCTTAAGCCATTCCTGTTTTTTTTTTT 7811

Qy 429 TTACATACTACCCGTCGATTCTAACTTCTTTCTTCTCTTGCCATCTTGCATTCTC 488
Db 7812 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTCTTCTTCTTCTTCTTCTTCTT 7871

RESULT 15
US-10-509-921-7
; Sequence 7, Application US/10509921
; Publication No. US20050250093A1

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; GENERAL INFORMATION:
; APPLICANT: SmithKline Beecham Corporation
; TITLE OF INVENTION: Hepatitis C Virus Sub-Genomic Replicons
; FILE REFERENCE: P51335
; CURRENT APPLICATION NUMBER: US/10/509,921
; CURRENT FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: 60/369,685
; PRIOR FILING DATE: 2002-04-03
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 7983
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Thepolynucleotide sequence encodes sequences from
; OTHER INFORMATION: HCV la Replicons
US-10-509-921-7

Query Match          0.8%; Score 30.4; DB 1; Length 7983;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
Matches 64; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

Qy 369 CCGAGGCCGAACGAGACAGACACACCATCATCATCAGCCATGCTTTTTTGTGATCGTTT 428
      |||||
Db 7755 CCGATGAAGTTGGGGTAAACACTCCGGCCTCTTAAGCCATTCCTGTTTTTTTTTTT 7814
      |||||

Qy 429 TTACATACTACCGTCGATTCCTAACCTTCCTTCTCTCTTGGCCATCTTTGCATCTC 488
      |||||
Db 7815 TTTTTTTTTTTTTTTCTTTTTTTTTTTCTTTCTCTTCTCTTTCTCTTTCTCTTTTC 7874
      |||||

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Search completed: November 24, 2005, 11:37:32  
Job time : 234 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: November 24, 2005, 01:34:24 ; Search time 661 Seconds  
(without alignments)  
10673.438 Million cell updates/sec

Title: US-10-066-007A-3

Perfect score: 3969  
Sequence: 1 cggaccgaacctcgccagc.....ttcatgtttgtcgactgcag 3969

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA:\*  
1: /cgn2\_6/ptodata/1/ina/1 COMB.seq:\*  
2: /cgn2\_6/ptodata/1/ina/5 COMB.seq:\*  
3: /cgn2\_6/ptodata/1/ina/6A COMB.seq:\*  
4: /cgn2\_6/ptodata/1/ina/6B COMB.seq:\*  
5: /cgn2\_6/ptodata/1/ina/H COMB.seq:\*  
6: /cgn2\_6/ptodata/1/ina/PPCTUS COMB.seq:\*  
7: /cgn2\_6/ptodata/1/ina/PP COMB.seq:\*  
8: /cgn2\_6/ptodata/1/ina/RE COMB.seq:\*  
9: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3969	100.0	3969	US-09-518-386B-4	Sequence 4, Appli
2	353.2	8.9	1932	US-09-518-386B-2	Sequence 2, Appli
3	82.8	2.1	7218	US-08-232-463-14	Sequence 14, Appl
C 4	47	1.2	300598	US-09-949-016-11868	Sequence 11868, A
C 5	47	1.2	302604	US-09-949-016-14588	Sequence 14588, A
C 6	47	1.2	302604	US-09-949-016-14589	Sequence 14589, A
C 7	47	1.2	308362	US-09-949-016-17119	Sequence 17119, A
8	46.8	1.2	832	US-09-621-976-2813	Sequence 2813, Ap
9	43.8	1.1	177251	US-09-949-016-15841	Sequence 15841, A
10	43.6	1.1	113701	US-09-949-016-13214	Sequence 13214, A
C 11	43	1.1	395	US-09-894-844-45	Sequence 45, Appl
C 12	43	1.1	1141	US-09-806-708B-22	Sequence 22, Appl
C 13	42.2	1.1	601	US-09-949-016-175160	Sequence 175160,
C 14	42	1.1	1141	US-09-806-708B-22	Sequence 22, Appl
C 15	41.2	1.0	13865	US-09-009-217-11	Sequence 11, Appl
C 16	41.2	1.0	13865	US-09-009-656-11	Sequence 11, Appl
C 17	41.2	1.0	13865	US-09-054-272-11	Sequence 11, Appl
C 18	41.2	1.0	16439	US-09-949-016-15745	Sequence 15745, A
C 19	40.8	1.0	601	US-09-949-016-201491	Sequence 201491,
C 20	40.8	1.0	86639	US-09-949-016-17397	Sequence 17397, A
21	40.6	1.0	15722	US-09-949-016-16709	Sequence 16709, A
C 22	40.4	1.0	289	US-09-007-005-17	Sequence 17, Appl
C 23	40.4	1.0	289	US-09-244-796-17	Sequence 17, Appl
C 24	40.2	1.0	34372	US-09-949-016-13098	Sequence 13098, A

C 25	40.2	1.0	34875	3	US-09-949-016-13099	Sequence 13099, A
C 26	39.4	1.0	7218	2	US-08-232-463-14	Sequence 14, Appl
C 27	39.2	1.0	12703	3	US-09-949-016-16685	Sequence 16685, A
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C 34	38.8	1.0	29927	3	US-09-949-016-17475	Sequence 17475, A
C 35	38.8	1.0	37802	3	US-09-949-016-12639	Sequence 12639, A
C 36	38.6	1.0	73519	3	US-09-949-016-16344	Sequence 16344, A
C 37	38.6	1.0	105919	3	US-09-949-016-11769	Sequence 11769, A
C 38	38.4	1.0	67479	3	US-09-949-016-11804	Sequence 11804, A
C 39	38.4	1.0	71119	3	US-09-949-016-15358	Sequence 15358, A
C 40	38.2	1.0	90541	3	US-09-759-359A-3	Sequence 3, Appli
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42	38	1.0	601	3	US-09-949-016-196595	Sequence 196595,
43	38	1.0	451924	3	US-09-949-016-12896	Sequence 12896, A
44	38	1.0	451925	3	US-09-949-016-17305	Sequence 17305, A
45	37.8	1.0	474	3	US-09-621-976-18033	Sequence 18033, A

ALIGNMENTS

RESULT 1  
US-09-518-386B-4  
; Sequence 4, Application US/09518386B  
; Patent No. 6365386  
; GENERAL INFORMATION:  
; APPLICANT: HOSHINO, Tatsuo  
; APPLICANT: OIIMA, Kazuyuki  
; APPLICANT: SETOGUCHI, Yutaka  
; TITLE OF INVENTION: ASTAXANTHIN SYNTHETASE  
; FILE REFERENCE: ASTAXANTHIN SYNTHETASE  
; CURRENT APPLICATION NUMBER: US/09/518,386B  
; CURRENT FILING DATE: 2000-03-03  
; PRIOR APPLICATION NUMBER: EP 99104668.1  
; PRIOR FILING DATE: 1999-03-09  
; PRIOR APPLICATION NUMBER: EP 00101666.6  
; PRIOR FILING DATE: 2000-02-01  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
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US-09-518-386B-4									
Query Match 100.0%; Score 3969; DB 3; Length 3969;									
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Matches 3969; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
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RESULT 2  
US-09-518-386B-2  
; Sequence 2, Application US/09518386B











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Qy 3102 GGACCAATTCAGCGTGTTCACACATCAATCGTTCAAAAGTTCAITTTATGAGAGATGAG 3161
Db 211 RNKYMSWHYHAMRYBKWABAVGCNNNNWKKORMAHHHWCATNNNNMMWYAYMHMHKKG 152
Qy 3162 AAGATTCAGGTACAATTCGTTTCTTTTAAAGCCCAATCGGT 3204
Db 151 AAWTNNKTABRDDHBAHVKTYYWRYDYWCAMCMWNAKAVRT 109
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## RESULT 13

```
US-09-949-016-175160/c
; Sequence 175160, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
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; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 175160
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-175160

Query Match 1.1%; Score 42.2; DB 3; Length 601;
Best Local Similarity 54.1%; Pred. No. 0.032;
Matches 86; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

Qy 408 ATGCTCTTTTGGGATCGTTTTTACATACTACCCGTCGATTCCTAACTCTTCTTCTTC 467
Db 382 AUGTAATTAATGTTTGGTTTTTTTCTTTCTTTCTTCTTCTTCTTCTTCTTCTTCTT 323
Qy 468 TCTTGCCATCTTTGCAATCTCTAATCTGTCGTGAACATCGATCCGATCTTTCGCCACTT 527
Db 322 TCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 263
Qy 528 TCTCCATATGTTTCATCTTGGTCTTGTCTCACAGTGCTTT 566
Db 262 TCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 224

RESULT 14
US-09-806-708B-22
; Sequence 22, Application US/09806708B
; Patent No. 6784342
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia
; TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
; FILE REFERENCE: 4810-58741
; CURRENT APPLICATION NUMBER: US/09/806,708B
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/147,133
; PRIOR FILING DATE: 1999-08-04
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 1141
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(1141)
; OTHER INFORMATION: consensus sequence of A.t., L.a., and B.n. FAEL promoters
US-09-806-708B-22

Query Match 1.1%; Score 42; DB 3; Length 1141;
Best Local Similarity 10.8%; Pred. No. 0.06;
Matches 96; Conservative 339; Mismatches 450; Indels 7; Gaps 4;

Qy 2510 AATTTCATGATCGACACGATATGCTAGCTGTGAGGATGTTTGTGATGCTAAATTC 2569
Db 61 WARMYCKYRRWYNNKSRWKWYKWKYBCANNYSRYHARRWKDKMTAYBMTMTNKWGK 120
Qy 2570 TTCTTCTGCAATGACTAAACCGGCTTCATCTTGTATCCATTTTAGAGAGCAACTTA 2629
Db 121 TGRHRYWRWABDVTDDHYYVTAMNNAWTTTCMDMDKDDKTRTWWKXNNNATGWDGDTK 180
Qy 2630 ATCGTTTGCCTATCTCGAAGGGTGTGCTGCTGCTTCTTGTCTTCTTCCAAATACA 2689
Db 181 YHWNNGGCTVWYRYKTDWBSKRMNYGMBWKNWSYDVYVWVDDMKCKRVRR 240
Qy 2690 ATACGGATTAATGCTCATCTGATTTGCTAGCGGCTGTGGAAATTAAGTTTGTTA 2749
Db 241 WVRTRGRMRNYMVABW-TAHRRRYNGWTBAMAYRRWNTWNNNNNAKAKCKRKYGNR 239
Qy 2750 AGGATCTCTTGTCTAGACCCCTCTAGTCCGCTAGTCCGCTAACCCTGTAATGCTTAAAGATG 2809
Db 300 ABVNSTCTWKSXTTKVRTSCWANNCRAGDANKDKWKKWKAAMGYVNNNNNNNTYKK 359
Qy 2810 AAGACGTATGTTGGCTTTCATCGACGATAATTTTTCATTTCTTCTTCTTGTACATACGCA 2869
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: November 21, 2005, 05:01:58 ; Search time 140 Seconds  
(without alignments)  
1813.897 Million cell updates/sec

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Perfect score: 1932  
Sequence: 1 gaattcgccagggccacc.....agccggctctgcccgaattc 1932

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3196817 seqs, 65720914 residues

Total number of hits satisfying chosen parameters: 6393634

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA New:  
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3: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB\_seq.\*  
4: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB\_seq.\*  
5: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB\_seq.\*  
6: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB\_seq.\*  
7: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB\_seq.\*  
8: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB\_seq.\*  
9: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB\_seq.\*  
10: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB\_seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41.4	2.1	2487	1	US-10-689-742-165
2	39	2.0	2030	1	US-10-652-893-3
3	38.8	2.0	2132	1	US-10-689-742-171
4	37.4	1.9	687	1	US-10-986-501-107
5	37.4	1.9	832	1	US-10-986-501-18
6	37.4	1.9	2298	1	US-10-689-742-69
7	37.2	1.9	3721	1	US-10-131-826A-543
8	37.2	1.9	3734	1	US-10-131-826A-147
9	37.2	1.9	340000	7	US-11-102-978-3
10	36.8	1.9	340000	7	US-11-102-978-3
11	36.6	1.9	2343	1	US-10-131-826A-107
12	36.6	1.9	3495	1	US-10-689-742-167
13	36.4	1.9	2276	1	US-10-131-826A-9
14	36.2	1.9	2625	7	US-11-102-978-12
15	36	1.9	1425	1	US-10-689-742-131
16	35.8	1.9	2719	1	US-10-652-893-1
17	35.6	1.8	1658	7	US-11-034-569-15
18	35.4	1.8	1968	1	US-10-131-826A-163
19	35.4	1.8	12482	9	US-11-090-878-25
20	35.4	1.8	55763	1	US-10-972-765-1
21	35	1.8	1687	1	US-10-131-826A-263
22	34.6	1.8	722	1	US-10-689-742-79
23	34.6	1.8	1257	1	US-10-689-742-115

24	34.6	1.8	1680	9	US-11-012-762-51	Sequence 51, Appl
25	34.6	1.8	1904	1	US-10-131-826A-99	Sequence 99, Appl
26	34.6	1.8	26000	1	US-10-949-720-391	Sequence 391, App
27	34.4	1.8	2845	1	US-10-131-826A-207	Sequence 207, App
28	34.4	1.8	2933	1	US-10-131-826A-345	Sequence 345, App
29	34.2	1.8	693	1	US-10-131-826A-499	Sequence 499, App
30	34.2	1.8	947	1	US-10-689-742-161	Sequence 161, App
31	34.2	1.8	1240	1	US-10-131-826A-91	Sequence 91, Appl
32	34.2	1.8	1714	1	US-10-131-826A-251	Sequence 251, App
33	34.2	1.8	2537	7	US-11-102-978-8	Sequence 8, Appli
34	34	1.8	600	1	US-10-986-501-60	Sequence 60, Appl
35	34	1.8	1624	1	US-10-131-826A-181	Sequence 181, App
36	34	1.8	1740	1	US-10-689-742-53	Sequence 53, Appl
37	34	1.8	1985	1	US-10-131-826A-143	Sequence 143, App
38	34	1.8	3501	1	US-10-131-826A-37	Sequence 37, Appl
39	33.8	1.7	1065	1	US-10-986-501-105	Sequence 105, App
40	33.8	1.7	4053	1	US-10-131-826A-351	Sequence 351, App
41	33.6	1.7	634	1	US-10-986-501-15	Sequence 15, Appl
42	33.6	1.7	680	1	US-10-526-716-3	Sequence 3, Appli
43	33.6	1.7	1346	1	US-10-131-826A-481	Sequence 481, App
44	33.4	1.7	496	1	US-10-131-826A-533	Sequence 533, App
45	33.2	1.7	640	1	US-10-986-501-57	Sequence 57, Appl

## ALIGNMENTS

RESULT 1  
US-10-689-742-165  
; Sequence 165, Application US/10689742  
; Publication No. US20050250180A1  
; GENERAL INFORMATION:  
; APPLICANT: Jacobs, Kenneth  
; APPLICANT: McCoy, John M  
; APPLICANT: LaValle, Edward R  
; APPLICANT: Racie, Lisa A  
; APPLICANT: Evans, Cheryl  
; APPLICANT: Merberg, David  
; APPLICANT: Treacy, Maurice  
; APPLICANT: Spaulding, Vikki  
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM  
; FILE REFERENCE: 00766.000091.10  
; CURRENT APPLICATION NUMBER: US/10/689,742  
; CURRENT FILING DATE: 2003-10-22  
; PRIOR APPLICATION NUMBER: 09/745,783  
; PRIOR FILING DATE: 2000-12-21  
; NUMBER OF SEQ ID NOS: 231  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 165  
; LENGTH: 2487  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-689-742-165

Query Match	2.1%	Score 41.4;	DB 1;	Length 2487;
Best Local Similarity	57.3%	Pred. No. 0.24;		
Matches	75;	Conservative	0;	Mismatches 55;
				Indels 0;
				Gaps 0;
QY	1771	TTTGTATCGATTGTGTTCTTCTACCCGGCGAGCGCTATGACTTCTACGTCTCTATCGT	1830	
Db	2271	TTTGTGTTTCACTGAATGTTCAATGTTTAAATGGCGATTAAATACTCTGCTGTATATAGT	2330	
QY	1831	CGCTCTGGACTCTTCTTACCTCTATATATTTCCATCCGAAAGAAAAA	1890	
Db	2331	AGTTTGTAGTAAATATTTTGAATAAAATCTGCCCGGATAAAAAA	2390	
QY	1891	AAAAA	1901	
Db	2391	AAAAA	2401	

RESULT 2  
US-10-652-893-3



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; PRIOR APPLICATION NUMBER: 60/056,371
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,732
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,366
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,364
; PRIOR FILING DATE: 1997-08-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 373
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 832
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-986-501-18
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Query Match 1.9%; Score 37.4; DB 1; Length 832;
Best Local Similarity 70.4%; Pred. No. 1.6; Indels 0; Gaps 0;
Matches 50; Conservative 0; Mismatches 21;

QY 1831 CGCTCTGACCTCTCTTACCTATATATTCATCCGAAAAA 1890
Db ||||| ||||| ||||| ||||| ||||| ||||| |||||
736 CGGCTGCGCCCTGCTGCCCAATAAAACCACTCCGACCCCAAAAAA 795
QY 1891 AAAAAA 1901
Db ||||| ||||| ||||| ||||| ||||| ||||| |||||
796 AAAAAA 806
```

```
RESULT 6
US-10-689-742-69
; Sequence 69, Application US/10689742
; Publication No. US20050250180A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M
; APPLICANT: Lavallie, Edward R
; APPLICANT: Racie, Lisa A
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Spaulding, Vikki
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: 00766.000091.10
; CURRENT APPLICATION NUMBER: US/10/689,742
; PRIOR FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: 09/746,783
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 69
; LENGTH: 2298
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-689-742-69
```

```
Query Match 1.9%; Score 37.4; DB 1; Length 2298;
Best Local Similarity 54.2%; Pred. No. 2.2; Indels 0; Gaps 0;
Matches 71; Conservative 2; Mismatches 58;

QY 1771 TTGTATCGATTGTTTCTCATACCGGCGAGCGGTATGACTTCTACGTCGCTATCGT 1830
Db ||||| ||||| ||||| ||||| ||||| ||||| |||||
2135 TTTCAAGCGATTGTGCTGTATAGGAAAAATGAGGGTTTACTTGTGCTTTCCATCA 2194
QY 1831 CGCTCTGACCTCTCTTACCTATATATTCATCCGAAAAA 1890
Db ||||| ||||| ||||| ||||| ||||| ||||| |||||
2195 CTATTTGCCATTAATAGGTGTCTTCACTCTTGCAAAAAA 2254
QY 1891 AAAAAA 1901
Db ||||| ||||| ||||| ||||| ||||| ||||| |||||
2255 AAAAAA 2265
```

```
RESULT 7
US-10-131-826A-543
; Sequence 543, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Deenoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 543
; LENGTH: 3721
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-131-826A-543
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```
Query Match 1.9%; Score 37.2; DB 1; Length 3721;
Best Local Similarity 54.3%; Pred. No. 2.9; Indels 0; Gaps 0;
Matches 75; Conservative 0; Mismatches 63;

QY 1761 CAATGCCCTTCTTTGTATCGATTGTTTCTCATACCGGCGAGCGGTATGACTTCTACGT 1820
Db ||||| ||||| ||||| ||||| ||||| ||||| |||||
3584 CTATGACCTTCAGCTGACCATGCATGCCACGTGGCTGGTGGTCTCTGCCCTCTTTGG 3643
QY 1821 CGTCTATCGTCGCTCTGGACTCTCTTCTTACCCCTATATATTTCCATCCGAAAAA 1880
Db ||||| ||||| ||||| ||||| ||||| ||||| |||||
3644 AGTTTGCCTCCCGAGCCCTCCCATCAATAAACTCTGTTTACACCAAAAAA 3703
QY 1881 AAAAAA 1898
Db ||||| ||||| ||||| ||||| ||||| ||||| |||||
3704 AAAAAA 3721
```





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; NAME/KEY: exon
; LOCATION: (167308)..(167438)
; OTHER INFORMATION: C21orf34 exon
; FEATURE:
; NAME/KEY: exon
; LOCATION: (216732)..(216833)
; OTHER INFORMATION: C21orf34 exon
US-11-102-978-3

Query Match      1.9%; Score 36.8; DB 7; Length 340000;
Best Local Similarity 69.4%; Pred. No. 16;
Matches 50; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

Qy 1835 CTGCACTCTCTTCCATCCCTATATATTTCCATCCGAAAAAAAAAAAAAAAAAAAAA 1894
Db 151459 CTGGATTATCTCATGTCTAATAGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 151518

Qy 1895 AAAAAAAGCGC 1906
Db 151519 AAAAAAAGGC 151530
```

```
RESULT 11
US-10-131-826A-107
; Sequence 107, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P330R1C128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 107
; LENGTH: 2343
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; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-131-826A-107

Query Match      1.9%; Score 36.6; DB 1; Length 2343;
Best Local Similarity 51.5%; Pred. No. 3.5;
Matches 84; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

Qy 1003 TGTCCGATGAGGAGTACTCGCTCAGATCAGTAACCTGTTATTGCTGGATATGAAACTT 1062
Db 1135 TCTCAGATATTGATGTACACTCTGAAGTGAAGCATTCTCTGTTGGCAGGACATGACACCT 1194
Qy 1063 CTTTCGACAGTCTTTCGACATGATGTTTTCACCGACTCTCAGAAAGCAAAAGCCGTTTCAGGATA 1122
Db 1195 TGGCAGCAAGCATCTCTCGATCCTTTACTGCTGCTCTGAACCTTGAGCATCAAGAGA 1254
Qy 1123 AACTTCGAGAAGAAATTTGTCAGATCGACACGAGTATGCTCTAC 1165
Db 1255 GATGCCGGAGGAGGTTCAGGGGCATCTCTGGGGGATGGTCTTTC 1297

RESULT 12
US-10-689-742-167
; Sequence 167, Application US/10689742
; Publication No. US20050250180A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M
; APPLICANT: LaVallie, Edward R
; APPLICANT: Racie, Lisa A
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Spaulding, Vikki
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: 00766.000091.10
; CURRENT APPLICATION NUMBER: US/10/689,742
; CURRENT FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: 09/746,783
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 167
; LENGTH: 3495
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-689-742-167

Query Match      1.9%; Score 36.6; DB 1; Length 3495;
Best Local Similarity 71.6%; Pred. No. 4;
Matches 48; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Qy 1835 CTGCACTCTCTTCCCTTACCCTATATATTTCCATCCGAAAAAAAAAAAAAAAAAAAAA 1894
Db 3414 CTTGACTATATGTTGTATTAAATTTGTTTACGAAAAAAAAAAAAAAAAAAAAA 3473

Qy 1895 AAAAAA 1901
Db 3474 AAAAAA 3480

RESULT 13
US-10-131-826A-9
; Sequence 9, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
```

APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Sherwood, Steven  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K  
APPLICANT: Wood, William  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3330R1C128  
CURRENT APPLICATION NUMBER: US/10/131,826A  
PRIORITY FILING DATE: 2002-04-24  
PRIOR APPLICATION NUMBER: 60/049911  
PRIOR FILING DATE: 1997-06-18  
PRIOR APPLICATION NUMBER: 60/056974  
PRIOR FILING DATE: 1997-08-26  
PRIOR APPLICATION NUMBER: 60/059113  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059115  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059117  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059122  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059184  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059263  
PRIOR FILING DATE: 1997-09-18  
PRIOR APPLICATION NUMBER: 60/059352  
PRIOR FILING DATE: 1997-09-19  
PRIOR APPLICATION NUMBER: 60/059588  
PRIOR FILING DATE: 1997-09-19  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 550  
SEQ ID NO 9  
LENGTH: 2276  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-131-826A-9

Query Match 1.9%; Score 36.4; DB 1; Length 2276;  
Best Local Similarity 87.0%; Pred. No. 3.8;  
Matches 40; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 1856 TATATTATTCATCCGAAAAA...AAAAAAAAAAAAAAAAAAAA 1901  
DB 2204 TATTTAATTCCTGCAAAAA...AAAAAAAAAAAAAAAAAAAA 2249

RESULT 14  
US-11-102-978-12  
Sequence 12, Application US/11102978  
Publication No. US20050250142A1  
GENERAL INFORMATION:  
APPLICANT: University of Utah Technology Transfer Office  
TITLE OF INVENTION: Diagnosis and Treatment of Herpes Simplex Virus Disease  
FILE REFERENCE: 0274-5537.IUS  
CURRENT APPLICATION NUMBER: US/11/102,978  
PRIORITY FILING DATE: 2005-04-11  
PRIOR APPLICATION NUMBER: PCT/US2003/033152  
PRIOR FILING DATE: 2003-10-18  
PRIOR APPLICATION NUMBER: 60/419,576  
PRIOR FILING DATE: 2002-10-18  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 12  
LENGTH: 2625  
TYPE: DNA  
ORGANISM: Homo sapiens

FEATURE:  
NAME/KEY: gene  
LOCATION: (1)..(2625)  
OTHER INFORMATION: CHODL  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (392)..(1213)  
OTHER INFORMATION: The gene is CHODL, encoding chondrolectin, NM024944.  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (506)..(928)  
OTHER INFORMATION: C-type lectin (CTL) or carbohydrate-recognition domain (CRD)  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (539)..(931)  
OTHER INFORMATION: C-type lectin (CTL) or carbohydrate-recognition domain (CRD)  
FEATURE:  
NAME/KEY: allele  
LOCATION: (1975)..(1975)  
OTHER INFORMATION: Comprises A or G.  
FEATURE:  
NAME/KEY: allele  
LOCATION: (2032)..(2032)  
OTHER INFORMATION: Comprises A or G.  
FEATURE:  
NAME/KEY: allele  
LOCATION: (2121)..(2121)  
OTHER INFORMATION: Comprises A or T.  
FEATURE:  
NAME/KEY: allele  
LOCATION: (2349)..(2349)  
OTHER INFORMATION: Comprises G or T.  
FEATURE:  
NAME/KEY: allele  
LOCATION: (2403)..(2404)  
OTHER INFORMATION: TCTA  
FEATURE:  
NAME/KEY: allele  
LOCATION: (2543)..(2543)  
OTHER INFORMATION: Comprises A or G.  
US-11-102-978-12

Query Match 1.9%; Score 36.2; DB 7; Length 2625;  
Best Local Similarity 60.8%; Pred. No. 4.5;  
Matches 59; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 1805 GCTATGACTTCTACGTCGTCTATCGTCCTGGACTCTCTTCTTACCCCTATATATT 1864  
DB 2474 GTTGTAACCTCTCGGTCTTCATATGTCCTGCTGCTCTTTAACCAATAAGAGTTCTT 2533  
QY 1865 CCATCGAAAAA...AAAAAAAAAAAAAAAAAAAA 1901  
DB 2534 GTTCTGAGAAAAA...AAAAAAAAAAAAAAAAAAAA 2570

RESULT 15  
US-10-689-742-131  
Sequence 131, Application US/10689742  
Publication No. US20050250180A1  
GENERAL INFORMATION:  
APPLICANT: Jacobs, Kenneth  
APPLICANT: McCoy, John M  
APPLICANT: LaVallie, Edward R  
APPLICANT: Racie, Lisa A  
APPLICANT: Evans, Cheryl  
APPLICANT: Merberg, David  
APPLICANT: Treacy, Maurice  
APPLICANT: Spaulding, Vikki  
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM  
FILE REFERENCE: 00766.000091.10  
CURRENT APPLICATION NUMBER: US/10/689,742  
CURRENT FILING DATE: 2003-10-22

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; PRIOR APPLICATION NUMBER: 09/746,783
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 131
; LENGTH: 1425
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-689-742-131
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Query Match      1.9%; Score 36; DB 1; Length 1425;
Best Local Similarity 80.8%; Pred. No. 4.1;
Matches 42; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 1850 ACCCTATATATTTCATCCGAAAAA 1901
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 1374 ACCCTGCTTTTGTTCAAAAA 1425
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
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Search completed: November 21, 2005, 07:30:18  
Job time : 142 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: November 21, 2005, 04:54:37 ; Search time 1091 Seconds  
(without alignments)  
14643.848 Million cell updates/sec

Title: US-10-066-007A-2

Perfect score: 1932

Sequence: 1 Gaattcgccagggccacc.....agccggctcgtcggaattc 1932

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA Main.\*

1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq.\*  
2: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq.\*  
3: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq.\*  
4: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq.\*  
5: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq.\*  
6: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq.\*  
7: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq.\*  
8: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq.\*  
9: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq.\*  
10: /cgn2\_6/ptodata/1/pubpna/US11\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1932	100.0	1932	5	US-10-066-007-2
2	353.2	18.3	3969	5	Sequence 2, Appli
3	51.8	2.7	702	8	Sequence 4, Appli
4	49.8	2.6	333	8	Sequence 3162, Ap
5	49.8	2.6	467	7	Sequence 54628, A
6	49.4	2.5	1501	6	Sequence 20949, A
7	49.2	2.5	368	7	Sequence 392, App
8	48.4	2.5	657	7	Sequence 1793, Ap
9	48.4	2.5	1458	8	Sequence 25496, A
10	48.4	2.5	1458	8	Sequence 1, Appli
11	48.4	2.5	1458	9	Sequence 1, Appli
12	48.4	2.5	1458	10	Sequence 1, Appli
13	48.4	2.5	1512	6	Sequence 55, Appl
14	48.4	2.5	1512	9	Sequence 407, App
15	48.4	2.5	2011	3	Sequence 1586, Ap
16	48.4	2.5	2059	7	Sequence 880-107-1586
17	48.4	2.5	2759	5	Sequence 1062, Ap
18	48.4	2.5	2768	6	Sequence 1, Appli
19	48.4	2.5	2768	6	Sequence 14, Appl
20	48.4	2.5	2768	6	Sequence 297, App
21	48.4	2.5	2849	3	Sequence 363, App
22	48.2	2.5	312	3	Sequence 2110, Ap
23	47.6	2.5	1400	10	Sequence 4611, Ap
					Sequence 1217, Ap

#### ALIGNMENTS

##### RESULT 1

US-10-066-007-2  
; Sequence 2, Application US/10066007  
; Publication No. US20030077691A1  
; GENERAL INFORMATION:  
; APPLICANT: HOSHINO, Tatsuo  
; APPLICANT: OJIMA, Kazuyuki  
; TITLE OF INVENTION: ASTAXANTHIN SYNTHETASE  
; FILE REFERENCE: ASTAXANTHIN SYNTHETASE  
; CURRENT APPLICATION NUMBER: US/10/066,007  
; CURRENT FILING DATE: 2001-02-01  
; PRIOR APPLICATION NUMBER: US/09/518,386  
; PRIOR FILING DATE: 2000-03-03  
; PRIOR APPLICATION NUMBER: EP 99104668.1  
; PRIOR FILING DATE: 1999-03-09  
; PRIOR APPLICATION NUMBER: EP 00101666.6  
; PRIOR FILING DATE: 2000-02-01  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 1932  
; TYPE: DNA  
; ORGANISM: Phaffia rhodozyma  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (33)..(1706)  
; NAME/KEY: polyA site  
; LOCATION: (1871)  
; NAME/KEY: mRNA  
; LOCATION: (14)..(1891)  
; US-10-066-007-2

Query Match 100.0%; Score 1932; DB 5; Length 1932;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1932; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GAATTCGGCAGGAGCCACCTTCTCCATATGTTTCATCTTGGTCTTGTCTCACAGTG 60  
Db 1 GAATTCGGCAGGAGCCACCTTCTCCATATGTTTCATCTTGGTCTTGTCTCACAGTG 60  
QY 61 CTTTAGGCTCGGCTGCTTTCTTCATGGGCATCCATAGCGTCTTTCAGTCTTTACCTCGGTC 120  
Db 61 CTTTAGGCTCGGCTGCTTTCTTCATGGGCATCCATAGCGTCTTTCAGTCTTTACCTCGGTC 120  
QY 121 CGAGCGCATCTTCACTGTATAACCTTCAGGGCCCGAATCATACCAACTACTTTACAGGCA 180

Sequence 5489, Ap  
Sequence 268, App  
Sequence 71313, A  
Sequence 29, Appl  
Sequence 41374, A  
Sequence 12, Appl  
Sequence 32438, A  
Sequence 162, App  
Sequence 33072, A  
Sequence 8656, Ap  
Sequence 75080, A  
Sequence 155277, A  
Sequence 23175, A  
Sequence 106, App  
Sequence 106, App  
Sequence 106, App  
Sequence 105, App  
Sequence 105, App  
Sequence 33549, A  
Sequence 72966, A  
Sequence 18917, A

Db	121	CGAGCGCATCTTCACTGTATAA	CTT	CAGGGCCCGAATCATACCA	CTACTTTTACAGCA	180
Qy	181	ATTTTTTAGACATCCTCTCAGCTCGTACAGGTGAAGAGCATCGCAAGTACAGAGAAAAT	240			
Db	181	ATTTTTTAGACATCCTCTCAGCTCGTACAGGTGAAGAGCATCGCAAGTACAGAGAAAAT	240			
Qy	241	ACGGAAGCACCTCCGGTTTCTCGGATCGGTGAGACCCCGTCTTGAACCTCGACCGATC	300			
Db	241	ACGGAAGCACCTCCGGTTTCTCGGATCGGTGAGACCCCGTCTTGAACCTCGACCGATC	300			
Qy	301	CGAAAGCTTTCAACCATGTGATGAAGAAGCTACGACTATCCGAAATCTGGTATGCGCG	360			
Db	301	CGAAAGCTTTCAACCATGTGATGAAGAAGCTACGACTATCCGAAATCTGGTATGCGCG	360			
Qy	361	CTCGAGTGTCTAGAAATTTGCTACCGGAGATGGTGTGTTACGGCGGAAGGTGAAGCTCAT	420			
Db	361	CTCGAGTGTCTAGAAATTTGCTACCGGAGATGGTGTGTTACGGCGGAAGGTGAAGCTCAT	420			
Qy	421	AGGACATCGAAGGATCATGATCCCTCTCTGTCGGCTCAGCCCGTTAAGTCGATGCTTC	480			
Db	421	AGGACATCGAAGGATCATGATCCCTCTCTGTCGGCTCAGCCCGTTAAGTCGATGCTTC	480			
Qy	481	CAATTTTTCTTAGAAAAAGGTATGAACTTTGTCGACAAAGATGATCGAGGATCGCGCTCAGA	540			
Db	481	CAATTTTTCTTAGAAAAAGGTATGAACTTTGTCGACAAAGATGATCGAGGATCGCGCTCAGA	540			
Qy	541	AGGATATGGCCGTGGGAGAGTCGGCCGGTGAAGAAAGGCAACAGACTCGAGACCGAAG	600			
Db	541	AGGATATGGCCGTGGGAGAGTCGGCCGGTGAAGAAAGGCAACAGACTCGAGACCGAAG	600			
Qy	601	GAGTCGATGTAAAGGATTTGGGTGGGTCTGAGCTACTCTTGGAGCTCATCGCTCTTGCAGGAT	660			
Db	601	GAGTCGATGTAAAGGATTTGGGTGGGTCTGAGCTACTCTTGGAGCTCATCGCTCTTGCAGGAT	660			
Qy	661	TTGACTATAAGAGCGACTCGCTCCAGAAACAGACTCTATGTGCGTCTTGTGCTG	720			
Db	661	TTGACTATAAGAGCGACTCGCTCCAGAAACAGACTCTATGTGCGTCTTGTGCTG	720			
Qy	721	GACTTACCGATGGTGTGCTCCTACCTTGGACTCGTTCAAGGCTCATCATGTGGATTTTG	780			
Db	721	GACTTACCGATGGTGTGCTCCTACCTTGGACTCGTTCAAGGCTCATCATGTGGATTTTG	780			
Qy	781	TACCTTACTTCCGAACCTATGAACCGGAGACATGAGATACCTTTGACTCAAGGATTTAGCAG	840			
Db	781	TACCTTACTTCCGAACCTATGAACCGGAGACATGAGATACCTTTGACTCAAGGATTTAGCAG	840			
Qy	841	TTTTCCGACGAGTTGGGATCGAGCTTATGGAGCAAAAGACGGCCGTCGTGGCTCAG	900			
Db	841	TTTTCCGACGAGTTGGGATCGAGCTTATGGAGCAAAAGACGGCCGTCGTGGCTCAG	900			
Qy	901	CTTCCGATCAGGCTGTGTGATAAAAAGGATGTTCAAGGTCGGGATATCCTAAGTCTCCTAG	960			
Db	901	CTTCCGATCAGGCTGTGTGATAAAAAGGATGTTCAAGGTCGGGATATCCTAAGTCTCCTAG	960			
Qy	961	TGAGAGCAAAACATCGCCGCCAAACCTGCTGAACTCTAAAAGCTGTCGATGAGAGGTAC	1020			
Db	961	TGAGAGCAAAACATCGCCGCCAAACCTGCTGAACTCTAAAAGCTGTCGATGAGAGGTAC	1020			
Qy	1021	TCGCTCAGATCAGTAACTGTTATTTCTCGATATGAACCTTCTTCGACAGTCTTTGACAT	1080			
Db	1021	TCGCTCAGATCAGTAACTGTTATTTCTCGATATGAACCTTCTTCGACAGTCTTTGACAT	1080			
Qy	1081	GGATGTTTACCAGCTCTCAGAAGCAAAAGCCGTTACAGGATAAACTTCGAGAGAAAATTT	1140			
Db	1081	GGATGTTTACCAGCTCTCAGAAGCAAAAGCCGTTACAGGATAAACTTCGAGAGAAAATTT	1140			
Qy	1141	GTCAAGTCGACAGGATATGCTTACGCTAGACGAACTTAATGCGTTCGCTTATCTCGAAG	1200			
Db	1141	GTCAAGTCGACAGGATATGCTTACGCTAGACGAACTTAATGCGTTCGCTTATCTCGAAG	1200			
Qy	1201	CGTTTGTAAAGGAGTCTCTTCTGCTAGACCCCTCTAGTTCGATATGCTTAAACCGTGAATGCT	1260			



```
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 20949
; LENGTH: 467
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_118922C.1
US-10-424-599-20949

Query Match      2.6%; Score 49.8; DB 7; Length 467;
Best Local Similarity 96.2%; Pred. No. 0.00053;
Matches 51; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1861 TATTCATCCGAGAAAAAAGCGCGCTCGA 1913
      |||||
Db 401 TATTCATCCAAAAAAGCGCGCTCGA 453

RESULT 6
US-10-264-237-392
; Sequence 392, Application US/10264237
; Publication No. US2004000949A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA131P1
; CURRENT APPLICATION NUMBER: US/10/264,237
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 392
; LENGTH: 1501
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (7)-(7)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-264-237-392

Query Match      2.6%; Score 49.4; DB 6; Length 1501;
Best Local Similarity 63.2%; Pred. No. 0.0014;
Matches 74; Conservative 1; Mismatches 42; Indels 0; Gaps 0;

Qy 1785 TTCTCATACCGGCGAGCGCTATGACTTCTAGTGTCTATCGTGTGCTGTGACTCTC 1844
      |||||
Db 1370 TTTTCTTGCTTGACTTGCTCTTTGTGCAGACTGCATTAAGTTGTGAGCTTGTGACTATC 1429

Qy 1845 TTCTTACCCTATATTTATTCATCCGAGAAAAAAGCGCGCTCGA 1901
      |||||
Db 1430 TTTTGAATAAGATTGATTTTAAACAAGAAAAAAGCGCGCTCGA 1486

RESULT 7
US-10-424-599-1793
; Sequence 1793, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
```

```
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 1793
; LENGTH: 368
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_101618C.1
US-10-424-599-1793

Query Match      2.5%; Score 49.2; DB 7; Length 368;
Best Local Similarity 87.1%; Pred. No. 0.00071;
Matches 54; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1853 CTATATATTTATTCATCCGAGAAAAAAGCGCGCTCG 1912
      |||||
Db 299 CAATAGATATTCATACCGAGAAAAAAGCGCGCTCT 358

Qy 1913 AG 1914
      ||
Db 359 AG 360

RESULT 8
US-10-424-599-25496/c
; Sequence 25496, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 25496
; LENGTH: 657
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_123024C.1
US-10-424-599-25496

Query Match      2.5%; Score 48.4; DB 7; Length 657;
Best Local Similarity 74.4%; Pred. No. 0.0017;
Matches 61; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

Qy 1833 CTCTGACTCTCTTCTTACCCCTATATATTTCCATCCGAGAAAAAAGCGCGCTCG 1892
      |||||
Db 91 CTCTGAGATTTCTCGAAAAACGATTCAGATGAAGAGAGCAAAAAAAGCGCGCTCT 32

Qy 1893 AAAAAAAGCGCGCTCGAG 1914
      |||||
Db 31 AAAAAAAGCGCGCTCTAG 10

RESULT 9
US-10-690-991-1
; Sequence 1, Application US/10690991
; Publication No. US2004024319A1
; GENERAL INFORMATION:
; APPLICANT: Tickle, Ian J
; APPLICANT: Vonrhein, Clemens
; APPLICANT: Williams, Pamela A
```



APPLICANT: Jhoti, Harren  
APPLICANT: Kirtson, Stewart Brian  
TITLE OF INVENTION: Crystal structure of cytochrome P450  
FILE REFERENCE: 620-282  
CURRENT APPLICATION NUMBER: US/10/690,991  
CURRENT FILING DATE: 2004-04-13  
PRIOR APPLICATION NUMBER: US 60/421,063  
PRIOR FILING DATE: 2002-10-25  
PRIOR APPLICATION NUMBER: PCT/GB02/02668  
PRIOR FILING DATE: 2002-05-30  
PRIOR APPLICATION NUMBER: US 10/221,036  
PRIOR FILING DATE: 2002-04-02  
PRIOR APPLICATION NUMBER: US 60/479,448  
PRIOR FILING DATE: 2003-06-19  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 1

LENGTH: 1458

TYPE: DNA

ORGANISM: Artificial sequence

FEATURE:

OTHER INFORMATION: Codes for SEQ ID NO: 2, a human 3A4 P450 protein truncated in its N-terminal region to delete the hydrophobic trans-membrane  
OTHER INFORMATION: domain, and the region replaced by a short N-terminal sequence.

US-10-690-991-1

Query Match 2.5%; Score 48.4; DB 8; Length 1458;

Best Local Similarity 50.7%; Pred. No. 0.0028;

Matches 146; Conservative 0; Mismatches 136; Indels 6; Gaps 1;

QY 997 AAAGCTTCGATGAGGAGTACTCGCTCAGATCAGTAACCTGTTATTTCTCGATATG 1056

Db 797 AAGCTCTGCGATGCGAGTCTGGGCCCCAATCAATTATCTTTATTTTCTGCTATG 856

QY 1057 AAACCTTCGACAGTCTTGACATGGATGTTTCCAGCACTCTCAGAGACAAAGCCGTTTC 1116

Db 857 AAACACAGCAGTGTCTCTCTTCATATGATGAATGGCCACTCACCTGATGTC 916

QY 1117 AGGATAAACTTCGAGAAGAAATTTGTTCAGATCGACACGGATATGCTTACGCTAGACGAAAC 1176

Db 917 AGCAGAACTGCAGGAGAAATTTGATGCAATTTTACCCCAATAAGGCCACCCACCTATG 976

QY 1177 TTAATGCGTTGC-----CTTATCTCGAAGGTTTGTAAAGAGTCTCTTCTGCTAGACC 1230

Db 977 ATACTGTCTACAGATGAGTATCTTGACATGGTGGTGAATGAACGCTCAGATTATTCC 1036

QY 1231 CTCCTAGTCCGATGCTTAACCGTGAATGCTTAAAGGATGAAGACTTCA 1278

Db 1037 CAATGCTATGAGACTTGAGGGGTCTGCNAAAAGATGTTGAGATCA 1084

RESULT 10

US-10-833-296-1

Sequence 1, Application US/10833296

Publication No. US20050032119A1

GENERAL INFORMATION:

APPLICANT: Tickler, Ian J

APPLICANT: Vinkovic, DiJana M

APPLICANT: Kirtson, Stewart

APPLICANT: Williams, Pamela A

APPLICANT: Jhoti, Harren

TITLE OF INVENTION: Crystal Structure of Cytochrome P450

FILE REFERENCE: 620-305

CURRENT APPLICATION NUMBER: US/10/833,296

CURRENT FILING DATE: 2004-04-28

PRIOR APPLICATION NUMBER: GB 0108214.8

PRIOR FILING DATE: 2001-04-02

PRIOR APPLICATION NUMBER: GB 0108212.2

PRIOR FILING DATE: 2001-04-02

PRIOR APPLICATION NUMBER: US 60/479,448

PRIOR FILING DATE: 2003-06-19

PRIOR APPLICATION NUMBER: US 60/421,063

PRIOR FILING DATE: 2002-10-25  
PRIOR APPLICATION NUMBER: US 60/306,873  
PRIOR FILING DATE: 2001-07-23  
PRIOR APPLICATION NUMBER: US 60/306,874  
PRIOR FILING DATE: 2001-07-23  
PRIOR APPLICATION NUMBER: US 10/690,991  
PRIOR FILING DATE: 2003-10-23  
PRIOR APPLICATION NUMBER: US 10/221,036  
PRIOR FILING DATE: 2002-04-02  
PRIOR APPLICATION NUMBER: PCT/GB02/02668  
PRIOR FILING DATE: 2002-05-30  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 1  
LENGTH: 1458  
TYPE: DNA  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: Codes for SEQ ID NO: 2, a human 3A4 P450 protein truncated in its N-terminal region to delete the hydrophobic trans-membrane  
OTHER INFORMATION: domain, and the region replaced by a short N-terminal sequence.

US-10-833-296-1

Query Match 2.5%; Score 48.4; DB 8; Length 1458;

Best Local Similarity 50.7%; Pred. No. 0.0028;

Matches 146; Conservative 0; Mismatches 136; Indels 6; Gaps 1;

QY 997 AAAGCTTCGATGAGGAGTACTCGCTCAGATCAGTAACCTGTTATTTCTCGATATG 1056

Db 797 AAGCTCTGCGATGCGAGTCTGGGCCCCAATCAATTATCTTTATTTTCTGCTATG 856

QY 1057 AAACCTTCGACAGTCTTGACATGGATGTTTCCAGCACTCTCAGAGACAAAGCCGTTTC 1116

Db 857 AAACACAGCAGTGTCTCTCTTCATATGATGAATGGCCACTCACCTGATGTC 916

QY 1117 AGGATAAACTTCGAGAAGAAATTTGTTCAGATCGACACGGATATGCTTACGCTAGACGAAAC 1176

Db 917 AGCAGAACTGCAGGAGAAATTTGATGCAATTTTACCCCAATAAGGCCACCCACCTATG 976

QY 1177 TTAATGCGTTGC-----CTTATCTCGAAGGTTTGTAAAGAGTCTCTTCTGCTAGACC 1230

Db 977 ATACTGTCTACAGATGAGTATCTTGACATGGTGGTGAATGAACGCTCAGATTATTCC 1036

QY 1231 CTCCTAGTCCGATGCTTAACCGTGAATGCTTAAAGGATGAAGACTTCA 1278

Db 1037 CAATGCTATGAGACTTGAGGGGTCTGCNAAAAGATGTTGAGATCA 1084

RESULT 11

US-10-516-338-7

Sequence 7, Application US/10516338

Publication No. US2005016434A1

GENERAL INFORMATION:

APPLICANT: Astex Technology Limited

APPLICANT: Cosme, Jose

APPLICANT: Ward, Alison

APPLICANT: Vuillard, Laurent

APPLICANT: Williams, Pamela

APPLICANT: Hamilton, Bruce

TITLE OF INVENTION: Methods of Purification of Cytochrome P450 Proteins

FILE REFERENCE: AHB06047252

CURRENT APPLICATION NUMBER: US/10/516,338

CURRENT FILING DATE: 2004-11-30

NUMBER OF SEQ ID NOS: 84

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 7

LENGTH: 1458

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: 3A4

US-10-516-338-7



; TITLE OF INVENTION: Cell Cycle Progression Proteins

; FILE REFERENCE: P015819WO CYK

; CURRENT APPLICATION NUMBER: US/10/745,237

; CURRENT FILING DATE: 2003-12-23

; PRIOR APPLICATION NUMBER: US 60/439,123

; PRIOR FILING DATE: 2003-01-10

; PRIOR APPLICATION NUMBER: US 60/468,402

; PRIOR FILING DATE: 2003-05-06

; NUMBER OF SEQ ID NOS: 600

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 407

; LENGTH: 1512

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION: M18907

US-10-745-237-407

Query Match 2.5%; Score 48.4; DB 9; Length 1512;

Best Local Similarity 50.7%; Pred. No. 0.0028; Mismatches 136; Indels 6; Gaps 1;

Matches 146; Conservative 0;

Qy 997 AAAAGCTGTCGATGAGGAGGTACTCGCTCAGATCAGTAACCTGTTATTTGCTGGATATG 1056

Db 863 AAGCTCTGTCGATCTGGAGCTCGTGCCCAATCAATTATCTTTATTTTGGCTGGCTATG 922

Qy 1057 AAATCTTCTCGACAGTCTTTGACATGGATGTTTCAACCGACTCTCAGAGACAAAGCCGTTT 1116

Db 923 AAACACGAGCAGTGTCTCTCTCTTCAATTATGTATGAACTGGCCCACTCACCCCTGATGTCC 982

Qy 1117 AGGATAAACTTCGAGAAGAAATTTGTGACATCGACACGGATATGCTACGCTAGACGAAAC 1176

Db 983 AGCAGAAACTCGAGGAGAAATTTGATGCAGTCTTACCAATAAGGCACACCCACCTATG 1042

Qy 1177 TTAATGCGTTGC-----CTTATCTCGAAGCGTTTGTAAAGGAGTCTCTTCGCTTAGAC 1230

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Qy 1231 CTCCTAGTCCGTATGCTTAACCGTGAATGCTTAAAGGATGAAGACTTCA 1278

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RESULT 15

US-09-880-107-1586

; Sequence 1586, Application US/09880107

; Patent No. US20020142981A1

; GENERAL INFORMATION:

; APPLICANT: Horne, Darci T.

; APPLICANT: Vockley, Joseph G.

; APPLICANT: Scherf, Uwe

; APPLICANT: Gene Logic, Inc.

; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer

; FILE REFERENCE: 44921-5028-WO

; CURRENT APPLICATION NUMBER: US/09/880,107

; CURRENT FILING DATE: 2001-06-14

; PRIOR APPLICATION NUMBER: US 60/211,379

; PRIOR FILING DATE: 2000-06-14

; PRIOR APPLICATION NUMBER: US 60/237,054

; PRIOR FILING DATE: 2000-10-02

; NUMBER OF SEQ ID NOS: 3950

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1586

; LENGTH: 2011

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION: Genbank Accession No. US20020142981A1 D00003

US-09-880-107-1586

Query Match

Best Local Similarity 2.5%; Score 48.4; DB 3; Length 2011;

Matches 146; Conservative 0; Mismatches 136; Indels 6; Gaps 1;

Qy 997 AAAAGCTGTCGATGAGGAGGTACTCGCTCAGATCAGTAACCTGTTATTTGCTGGATATG 1056

Db 926 AAGCTCTGTCGATCTGGAGCTCGTGCCCAATCAATTATCTTTATTTTGGCTGGCTATG 985

Qy 1057 AAACTTCTTCGACAGTCTTGACATGGATGTTTCAACCGACTCTCAGAGACAAAGCCGTTT 1116

Db 986 AAACACGAGCAGTGTCTCTCTCTTCAATTATGTATGAACTGGCCCACTCACCCCTGATGTCC 1045

Qy 1117 AGGATAAACTTCGAGAAGAAATTTGTGACATCGACACGGATATGCTACGCTAGACGAAAC 1176

Db 1046 AGCAGAAACTCGAGGAGAAATTTGATGCAGTCTTACCCAATAAGGCACACCCACCTATG 1105

Qy 1177 TTAATGCGTTGC-----CTTATCTCGAAGCGTTTGTAAAGGAGTCTCTTCGCTTAGAC 1230

Db 1106 ATACTGTCTACAGATGGAGTATCTTGACATGGTGTGATGAACGCTCAGATTATTTC 1165

Qy 1231 CTCCTAGTCCGTATGCTTAACCGTGAATGCTTAAAGGATGAAGACTTCA 1278

Db 1166 CAATTGCTATGAGACTTGGAGGGTCTGCAAAAAAGATGTTGAGATCA 1213

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Job time : 1093 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 21, 2005, 02:44:22 ; Search time 261 Seconds  
(without alignments)

13158.043 Million cell updates/sec

Title: US-10-066-007A-2

Perfect score: 1932  
Sequence: 1 gaattcgccagcaggccacc.....agcggctgtgcgaattc 1932

Scoring table: IDENTITY NUC

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Searched: 1303057 seqs, 888780828 residues

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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8: /cgn2\_6/ptodata/1/ina/RE-COMB.seq.\*  
9: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1932	100.0	1932	3	US-09-518-386B-2
2	353.2	18.3	3969	3	US-09-518-386B-4
3	48.4	2.5	1512	3	US-08-277-031B-4
4	48.4	2.5	2059	3	US-09-023-655-1062
5	48.4	2.5	2079	3	US-09-949-016-2691
6	48.4	2.5	2759	3	US-09-144-367-1
7	48.4	2.5	2768	3	US-09-949-016-1221
8	47.4	2.5	2160	3	US-09-716-129-12
9	46.8	2.4	1712	3	US-09-148-545-106
10	46.8	2.4	1712	3	US-09-621-011-106
11	46.8	2.4	1822	3	US-09-148-545-105
12	46.8	2.4	1822	3	US-09-621-011-105
13	45.2	2.3	2080	3	US-09-949-016-2690
14	45	2.3	1831	3	US-08-948-564-15
15	44.8	2.3	1801	3	US-09-709-103-3
16	44.8	2.3	1801	3	US-09-439-410A-3
17	44	2.3	3828	3	US-09-221-013A-7
18	43.6	2.3	352	3	US-09-144-367-8
19	43.6	2.3	31197	3	US-09-949-016-12963
20	43.6	2.3	103934	3	US-09-949-016-14433
21	42.8	2.2	1333	3	US-09-372-422A-9
22	42.8	2.2	2407	3	US-09-370-807-7
23	42.8	2.2	2407	3	US-09-921-259-7
24	42.6	2.2	84252	3	US-09-949-016-17315

25	42.6	2.2	246240	2	US-08-724-394A-20	Sequence 20, Appl
26	42.6	2.2	246240	2	US-08-724-394A-21	Sequence 21, Appl
27	42.6	2.2	246240	2	US-08-724-394A-22	Sequence 22, Appl
C 28	42.4	2.2	396	3	US-09-840-173-19	Sequence 19, Appl
C 29	42.4	2.2	396	3	US-09-713-550-19	Sequence 19, Appl
C 30	42.4	2.2	396	3	US-09-825-294-19	Sequence 19, Appl
C 31	42.4	2.2	396	3	US-09-970-966-19	Sequence 19, Appl
C 32	42.4	2.2	10980	3	US-09-949-016-14471	Sequence 14471, A
C 33	42.4	2.2	15584	3	US-09-949-016-12783	Sequence 12783, A
C 34	42.2	2.2	47	2	US-08-778-494B-114	Sequence 114, App
C 35	42.2	2.2	323	3	US-09-621-976-10374	Sequence 10374, A
36	42.2	2.2	883	3	US-10-088-092A-14	Sequence 14, Appl
37	41.6	2.2	2202	3	US-09-396-149-3	Sequence 3, Appl
38	41.6	2.2	2691	3	US-10-101-464A-837	Sequence 837, App
C 39	41.6	2.2	41895	3	US-09-949-016-15135	Sequence 15135, A
C 40	41.6	2.2	199945	3	US-09-949-016-15436	Sequence 15436, A
41	41.4	2.1	1126	3	US-09-389-956-7	Sequence 7, Appl
42	41.4	2.1	1507	3	US-09-453-323-1	Sequence 1, Appl
43	41.4	2.1	2059	3	US-09-949-016-5390	Sequence 5390, Ap
C 44	41.4	2.1	7218	2	US-08-232-463-14	Sequence 14, Appl
45	41.2	2.1	824	3	US-10-144-929-29	Sequence 29, Appl

#### ALIGNMENTS

##### RESULT 1

US-09-518-386B-2  
; Sequence 2, Application US/09518386B  
; Patent No. 6365386  
; GENERAL INFORMATION:  
; APPLICANT: HOSHINO, Tateuo  
; APPLICANT: OJIMA, Kazuyuki  
; APPLICANT: SETOGUCHI, Yutaka  
; TITLE OF INVENTION: ASTAXANTHIN SYNTHETASE  
; FILE REFERENCE: ASTAXANTHIN SYNTHETASE  
; CURRENT APPLICATION NUMBER: US/09/518,386B  
; CURRENT FILING DATE: 2000-03-03  
; PRIOR APPLICATION NUMBER: EP 99104668.1  
; PRIOR FILING DATE: 1999-03-09  
; PRIOR APPLICATION NUMBER: EP 00101666.6  
; PRIOR FILING DATE: 2000-02-01  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 1932  
; TYPE: DNA  
; ORGANISM: Phaffia rhodozyma  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (33)..(1706)  
; NAME/KEY: polyA\_site  
; LOCATION: (1871)  
; NAME/KEY: mRNA  
; LOCATION: (14)..(1891)  
; US-09-518-386B-2

Query Match 100.0%; Score 1932; DB 3; Length 1932;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1932; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY	61	CTTTAGGCTCGCTGCTTTCTCATGGGCATCCATAGCGTTCTTTCAGTCTTTTACCTCGTCTC	120
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QY	121	CGAGCGCATCTTCACTGTATAACCTTCAGGCGCCGAATCATACCACTACTTTTACAGCA	180
Db	121	CGAGCGCATCTTCACTGTATAACCTTCAGGCGCCGAATCATACCACTACTTTTACAGCA	180

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1801 AGCGCTATGACTTCTACGCTCTATCGCTCTGCTGCTGAGACTCTTCTTACCCATATAT 1860  
1861 TATTCATCCGAAAAA 1932  
1921 CGTGCCGAATTC 1932  
1921 CGTGCCGAATTC 1932

## RESULT 2

US-09-518-386B-4  
; Sequence 4, Application US/09518386B  
; Patent No. 6365386  
; GENERAL INFORMATION:  
; APPLICANT: HOSHINO, Tatsuo  
; APPLICANT: OJIMA, Kazuyuki  
; APPLICANT: SETOGUCHI, Yutaka  
; TITLE OF INVENTION: ASTAXANTHIN SYNTHETASE  
; FILE REFERENCE: ASTAXANTHIN SYNTHETASE  
; CURRENT APPLICATION NUMBER: US/09/518,386B  
; CURRENT FILING DATE: 2000-03-03  
; PRIOR APPLICATION NUMBER: EP 99104668.1  
; PRIOR FILING DATE: 1999-03-09  
; PRIOR APPLICATION NUMBER: EP 00101666.6  
; PRIOR FILING DATE: 2000-02-01  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 3969  
; TYPE: DNA  
; ORGANISM: Phaffia rhodozyma  
; FEATURE:  
; NAME/KEY: 5'UTR  
; LOCATION: (517)..(518)

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; NAME/KEY: intron
; LOCATION: (784)..(898)
; NAME/KEY: intron
; LOCATION: (1016)..(1087)
; NAME/KEY: intron
; LOCATION: (1180)..(1302)
; NAME/KEY: intron
; LOCATION: (1518)..(1600)
; NAME/KEY: intron
; LOCATION: (1635)..(1723)
; NAME/KEY: intron
; LOCATION: (1867)..(1939)
; NAME/KEY: intron
; LOCATION: (2000)..(2081)
; NAME/KEY: intron
; LOCATION: (2182)..(2257)
; NAME/KEY: intron
; LOCATION: (2355)..(2431)
; NAME/KEY: intron
; LOCATION: (2543)..(2618)
; NAME/KEY: intron
; LOCATION: (2653)..(2742)
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; LOCATION: (2815)..(2962)
; NAME/KEY: intron
; LOCATION: (3051)..(3113)
; NAME/KEY: intron
; LOCATION: (3172)..(3247)
; NAME/KEY: intron
; LOCATION: (3322)..(3398)
; NAME/KEY: intron
; LOCATION: (3424)..(3513)
; NAME/KEY: polyA site
; LOCATION: (3865)..(3866)
; NAME/KEY: intron
; LOCATION: (653)..(734)
; LOCATION: 518-386B-4
US-09-518-386B-4
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Query Match 18.3%; Score 353.2; DB 3; Length 3969;
Best Local Similarity 99.2%; Pred. No. 1.3e-96;
Matches 355; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1514 TTGCTTTGGTGGCGATTTGCTGCGCGAGATGAAGCCCTCTTTGTTGTCACCTCTCCG 1573
Db 3508 TCGCAGTGGTGGCGATTTGCTGCGCGAGATGAAGCCCTCTTTGTTGTCACCTCTCCG 3567

Qy 1574 TCGGCTCCAGTTCGAGCCCATCATCTCTCATCCAGATACGAGCACATCACCTTCATCAT 1633
Db 3568 TCGGCTCCAGTTCGAGCCCATCATCTCTCATCCAGATACGAGCACATCACCTTCATCAT 3627

Qy 1634 TTCCCGTCTCGAATCGTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1693
Db 3628 TTCCCGTCTCGAATCGTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 3687

Qy 1694 GCGGTCGATGAGTTGATCTTCATATCTTAAGAGAGTTCATATCTGAGAAATGTGTG 1753
Db 3698 GCGGTCGATGAGTTGATCTTCATATCTTAAGAGAGTTCATATCTGAGAAATGTGTG 3747

Qy 1754 ACTAGACAAATCCCTTTCTTTGATCGATTTGTTCTCATACCGGCGAGGCGCTATGACT 1813
Db 3748 ACTAGACAAATCCCTTTCTTTGATCGATTTGTTCTCATACCGGCGAGGCGCTATGACT 3807

Qy 1814 TCTAGTCGTCTATCGTCGCTCTGACTCTCTTCTTACCTATATATTTATTCATCCG 1871
Db 3808 TCTAGTCGTCTATCGTCGCTCTGACTCTCTTCTTACCTATATATTTATTCATCCG 3865
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## RESULT 3

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US-08-277-031B-4
; Sequence 4, Application US/08277031B
; Patent No. 6620593
; GENERAL INFORMATION:
; APPLICANT: Hayashi, Koji
```

```
; APPLICANT: Sakaki, Toshiyuki
; APPLICANT: Yabusaki, Yoshiyasu
; APPLICANT: Komai, Koichiro
; APPLICANT: Kaneko, Hideo
; APPLICANT: Nakatsuka, Iwao
; TITLE OF INVENTION: METHOD FOR SAFETY EVALUATION OF
; TITLE OF INVENTION: CHEMICAL COMPOUND USING RECOMBINANT YEAST EXPRESSING
; TITLE OF INVENTION: HUMAN CYTOCHROME P450
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch
; STREET: P.O. Box 747
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5inch, 1.44MB
; COMPUTER: IBM PC
; OPERATING SYSTEM: Dos 5.0
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/277,031B
; FILING DATE: 19-JULY-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP-201120/1993
; APPLICATION NUMBER: JP-180246/1993
; APPLICATION NUMBER: JP-208279/1993
; FILING DATE: 20-07-1993
; FILING DATE: 21-07-1993
; FILING DATE: 30-07-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Raymond C. Stewart
; REGISTRATION NUMBER: 21,066
; REFERENCE/DOCKET NUMBER: 20-3530P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-205-8000
; TELEFAX: 703-205-8050
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1512
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; US-08-277-031B-4

Query Match 2.5%; Score 48.4; DB 3; Length 1512;
Best Local Similarity 50.7%; Pred. No. 0.00078;
Matches 146; Conservative 0; Mismatches 136; Indels 6; Gaps 1;

Qy 997 AAAAGCTGTCGATGAGGAGGTACTCGCTCAGATCAGTAACCTGTTATTGCTGGATATG 1056
Db 863 AAGCTCTGTCGATCTCGAGCTCGTGGCCCAATCAATTATCTTTATTTTCTGGCTATG 922

Qy 1057 AAATCTTTCACAGCTTTGACATGGATGTTTACCAGACTCTCAGACAGCAAGCCGTTCC 1116
Db 923 AAACCCAGCAGCTGTTCTCTCTTCATTATGTATGAACCTGGCACTCACCCTGATGTCC 982

Qy 1117 AGGATAAACTTCGAGAGAAAATTTGTCCAGATCGACAGGATATGCTACGCTAGACGAAC 1176
Db 983 AGCAGAACTTCGAGAGAAAATTTGTCCAGATCGACAGGATATGCTACGCTAGACGAAC 1042

Qy 1177 TTAATGCGTTGC-----CTTATCTCGAAGCGTTGTTTAAGAGGTCCTCTTCTGCTAGACC 1230
Db 1043 ATACTGTCTACAGATGGAGTATCTTGACATGGTGGTGAATGAAACGCTCAGATTATTCC 1102

Qy 1231 CTCCTAGTCCGTTATGCTTAACCGTGAATGCTTTAAAGGATGAAGACTTCA 1278
Db 1103 CAATTGCTATGAGACTTGAGAGGGGTCTGCAAAAAGATGTTGAGATCA 1150
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Query Match	2.5%; Score 48.4; DB 3; Length 2059;	
Best Local Similarity	50.7%; Pred. No. 0.00095;	
Matches 146; Conservative	0; Mismatches 136; Indels	6; Gaps
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Db		
Qy	953 AAGTCTCTCGGATCTGGAGCTCGTGGCCCAATCAATTATCTTATTTTGGCTGGCTATG	1012
Db		
Qy	1057 AAATCTCTTCGACAGCTCTTGACATGGATGTTTCACCGACTCTCAGACAGACAAGCCGTTTC	1116
Db		
Qy	1013 AAACACGAGCAGTGTTCTCTCTCTTCATATGTATGAACTGGCCCACTCACCGCTGATGTCC	1072
Db		
Qy	1117 AGGATAAACTTCGAGAGAAGAAATTTGTCAGATCGACACGGATATGCTACGCTAGACGAC	1176
Db		
Qy	1073 AGCAGAACTCCAGGAGGAATTTGATGTCAGTCTTTACCCAAATAGGCAACACCCACTATG	1132
Db		
Qy	1177 TTAATGCGTTGC-----CTTATCTCGAAGCGTTTCTTAAGGAGTCTCTTGCTCTAGACC	1230
Db		
Qy	1133 ATACTGTCTACAGATCGAGTATCTTGCATGTGTGTGAATCAAGCGTTCAGATTATTC	1192
Db		
Qy	1231 CTCCTAGTCCGTATGCTAAACGGTGAATGCTTAAAGATGAAGACTTCA	1278
Db		
Qy	1193 CAATTGCTATGAGACTTTGAGAGGGTCTGCAAAAAGATGTTGAGATCA	1240
Db		

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RESULT 5
US-09-949-016-2691
; Sequence 2691, Application US/09949016
; Patent No. 681239
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 2691
; LENGTH: 2079
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-2691

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Query March	2.5%;	Score 48.4;	DB 3;	Length 2079;
Best Local Similarity	50.7%;	Pred. No. 0.00095;		
Matches 146;	Conservative 0;	Mismatches 136;	Indels 6;	Gaps 1;
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Db	968	AAGCTCTGTCGAGTCTGAGACTCGTGCCCAATATCTTATTTTCTGGCTATG	1027	
Qy	1057	AAACTTCTTCGACAGCTTGACATGGATGTTTCACCGACTCTCAGAAGACAAAGCCGTTTC	1116	
Db	1028	AAACACGACGAGTGTTCTCTCTCATTAATGATGAACTGGCCACTCACCCCTGATGTCC	1087	
Qy	1117	AGGATAAAGCTTCGAGAAGAAATTTGTGCAGATCGACACGGATATGCCTACGCTAGACGAAC	1176	
Db	1088	AGCAGAAACTGACAGGAGGAAATTTGATGCAAGTTTATCCCAATAAGGACACCAACCACCTATG	1147	
Qy	1177	TTAATGGTTGC-----CTTATCTCGAAGCGTTTGTTAAGGAGTCTCTTCGCTAGACC	1230	
Db	1148	ATACTGTGCTACAGATGGAGTATCTTGACATGCTGTGTGAATGAACGCTCAGATTATTTCC	1207	
Qy	1231	CTCCTAGTCGGTATGCTAACCGTGAATGCTTTAAGGATGAAGACTTCA	1278	
Db	1208	CAATTGCTATGACACTTGAGAGGGCTTCGAAAAGATGTTTGAGATCA	1255	

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RESULT 6
US-09-144-367-1
; Sequence 1, Application US/09144367
; Patent No. 6432639
; GENERAL INFORMATION:
; APPLICANT: Lichter, Jay
; APPLICANT: Guido, Marco
; TITLE OF INVENTION: GENOTYPING OF HUMAN CYP3A4
; FILE REFERENCE: SEQ-12P
; CURRENT APPLICATION NUMBER: US/09/144,367
; CURRENT FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 60/058,612
; PRIOR FILING DATE: 1997-09-10
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 2759
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (70) ... (1581)

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/ EARLIER APPLICATION NUMBER: 60/056,877  
 / EARLIER FILING DATE: 1997-08-22  
 / EARLIER APPLICATION NUMBER: 60/056,889  
 / EARLIER FILING DATE: 1997-08-22  
 / EARLIER APPLICATION NUMBER: 60/056,893  
 / EARLIER FILING DATE: 1997-08-22  
 / EARLIER APPLICATION NUMBER: 60/056,630  
 / EARLIER FILING DATE: 1997-08-22  
 / EARLIER APPLICATION NUMBER: 60/056,878  
 / EARLIER FILING DATE: 1997-08-22  
 / EARLIER APPLICATION NUMBER: 60/056,662  
 / EARLIER FILING DATE: 1997-08-22  
 / EARLIER APPLICATION NUMBER: 60/056,872  
 / EARLIER FILING DATE: 1997-08-22  
 / EARLIER APPLICATION NUMBER: 60/056,882  
 / EARLIER FILING DATE: 1997-08-22  
 / EARLIER APPLICATION NUMBER: 60/056,637  
 / EARLIER FILING DATE: 1997-08-22  
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 / EARLIER FILING DATE: 1997-08-22  
 / EARLIER APPLICATION NUMBER: 60/056,888  
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 / EARLIER FILING DATE: 1997-08-22  
 / EARLIER APPLICATION NUMBER: 60/056,845  
 / EARLIER FILING DATE: 1997-08-22  
 / EARLIER APPLICATION NUMBER: 60/056,892  
 / EARLIER FILING DATE: 1997-08-22  
 / EARLIER APPLICATION NUMBER: 60/047,595  
 / EARLIER FILING DATE: 1997-05-23  
 / EARLIER APPLICATION NUMBER: 60/057,761  
 / EARLIER FILING DATE: 05-Sep-1997  
 / EARLIER APPLICATION NUMBER: 60/047,599  
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 / EARLIER FILING DATE: 1997-05-23  
 / EARLIER APPLICATION NUMBER: 60/047,586  
 / EARLIER FILING DATE: 1997-05-23  
 / EARLIER APPLICATION NUMBER: 60/047,590  
 / EARLIER FILING DATE: 1997-05-23  
 / EARLIER APPLICATION NUMBER: 60/047,594  
 / EARLIER FILING DATE: 1997-05-23  
 / EARLIER APPLICATION NUMBER: 60/047,589  
 / EARLIER FILING DATE: 1997-05-23  
 / EARLIER APPLICATION NUMBER: 60/047,593  
 / EARLIER FILING DATE: 1997-05-23  
 / EARLIER APPLICATION NUMBER: 60/047,614  
 / EARLIER FILING DATE: 1997-05-23  
 / EARLIER APPLICATION NUMBER: 60/043,578  
 / EARLIER FILING DATE: 1997-04-11  
 / EARLIER APPLICATION NUMBER: 60/043,576  
 / EARLIER FILING DATE: 1997-04-11  
 / EARLIER APPLICATION NUMBER: 60/047,501  
 / EARLIER FILING DATE: 1997-05-23  
 / EARLIER APPLICATION NUMBER: 60/043,670

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; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/056,632
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; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,862
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,887
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,908
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 280
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 106
; LENGTH: 1712

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Best Local Similarity 85.0%; Pred. No. 0.0026;
Matches 51; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 1854 TATATATTATTCATCCGAAAAAAGCGCCGCTCGA 1913
DB 1645 TAAATATATTTTGTACAAAAAAGCGCCGCTCGA 1704

RESULT 10
US-09-621-011-106
; Sequence 106, Application US/09621011
; Patent No. 6878687
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 70 Human Secreted Proteins
; FILE REFERENCE: P2001P1
; CURRENT APPLICATION NUMBER: US/09/621,011
; PRIOR application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 280
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 106
; LENGTH: 1712
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-621-011-106

Query Match      2.4%; Score 46.8; DB 3; Length 1712;
Best Local Similarity 85.0%; Pred. No. 0.0026;
Matches 51; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 1854 TATATATTATTCATCCGAAAAAAGCGCCGCTCGA 1913
DB 1645 TAAATATATTTTGTACAAAAAAGCGCCGCTCGA 1704

RESULT 11
US-09-148-545-105
; Sequence 105, Application US/09148545
; Patent No. 6590075
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 70 Human Secreted Proteins
; FILE REFERENCE: P2001P1
; CURRENT APPLICATION NUMBER: US/09/148,545
; PRIOR application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 280
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 105
; LENGTH: 1712
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-148-545-105
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; EARLIER APPLICATION NUMBER: 60/056,880  
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; EARLIER APPLICATION NUMBER: 60/056,894  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,911  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,636  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,874  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,910  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,864  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,631  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,845  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,892  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/047,595  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/057,761  
; EARLIER FILING DATE: 05-Sep-1997  
; EARLIER APPLICATION NUMBER: 60/047,599  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,588  
; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,585  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,586  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,590  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,594  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,589  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,593  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,614  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/043,578  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,576  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/047,501  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/043,670  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/056,632  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,664  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,876  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,881  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,909  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,875  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,862  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,887  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,908  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/048,964  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/057,650  
; EARLIER FILING DATE: 1997-09-05  
; EARLIER APPLICATION NUMBER: 60/056,884  
; EARLIER FILING DATE: 1997-08-22  
; NUMBER OF SEQ ID NOS: 280  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 105  
; LENGTH: 1822

Query Match 2.4%; Score 46.8; DB 3; Length 1822;  
Best Local Similarity 85.0%; Pred. No. 0.0027;  
Matches 51; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

Oy 1854 TATATATTATTCATCCGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGCGCGCTCGA 1913  
Db 1755 TAAATATATTTTGTACAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGSGCGCTCGA 1814

## RESULT 12

US-09-621-011-105  
; Sequence 105, Application US/09621011  
; Patent No. 6878687  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: 70 Human Secreted Proteins  
; FILE REFERENCE: P2001P1  
; CURRENT APPLICATION NUMBER: US/09/621,011  
; CURRENT FILING DATE: 2000-07-20  
; Prior application data removed - consult PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 280  
; SOFTWARE: PatentIn Ver. 2.0

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; SEQ ID NO 105
; LENGTH: 1822
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-011-105

Query Match      2.4%; Score 46.8; DB 3; Length 1822;
Best Local Similarity 85.0%; Pred. No. 0.0027;
Matches 51; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

Qy 1854 TATATATTATCCATCCGAAAAAAGGCGCGCTCGA 1913
Db 1755 TAAATATATTTTGTACAAAAAAGGCGCGCTCGA 1814

RESULT 13
US-09-949-016-2690
; Sequence 2690, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2690
; LENGTH: 2080
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-2690

Query Match      2.3%; Score 45.2; DB 3; Length 2080;
Best Local Similarity 50.0%; Pred. No. 0.009;
Matches 144; Conservative 0; Mismatches 138; Indels 6; Gaps 1;

Qy 997 AAAAGCTCTCCGATGAGGAGTCTCGCTCAGATCAGTAACCTGTTATTGCTGGATATG 1056
Db 968 AAGCTCTCTGATCTGAGCTCATGGCCCAATCAATATCTTTATTGCTGGCTATG 1027
Qy 1057 AAATCTCTTCGACGCTTGACATGGATGTTTCACCGACTCTCAGAACAAAGCCGTTCC 1116
Db 1028 AAACACGAGCAGTGTCTCTCTTCATATATATGAATGCGCACTCACCCCTGATGTCC 1087
Qy 1117 AGGATAAATCTCGAAGAAATTTCTCAGATCGACACGATATGCTACGCTAGACGAAC 1176
Db 1088 AGCAGAAATGAGAGAAATGATGATGATGATGATGATGATGATGATGATGATGATG 1147
Qy 1177 TTAATGC-----GTTGCTTATCTCGAAGCGTTTGTAAAGAGTCTCTTGTCTAGACC 1230
Db 1148 ATACTGTGTACAGTTGGAGTATCTTGACATGGTGTGAATGAAACACTCAGATTATTC 1207
Qy 1231 CTCCTAGTCCGATGCTACCGTGAATGCTTAAAGATGAGACTTCA 1278
Db 1208 CAGTTGCTATGAGACTTGAGAGGGTCTGCAAAAAAGATGTTGAAATCA 1255

RESULT 14
US-08-948-564-15
; Sequence 15, Application US/08948564
; Patent No. 6121512
; GENERAL INFORMATION:
; APPLICANT: Siminszky, Balazs
; APPLICANT: Dewey, Ralph E.
; APPLICANT: Corbin, Frederick T.
```

```
; TITLE OF INVENTION: No. 6121512el Cytochrome P-450 Constructs and
; TITLE OF INVENTION: Methods of Producing Herbicide-Resistant Transgenic Plants
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Virginia C. Bennett
; STREET: PO Box 37428
; CITY: Raleigh
; STATE: No. 6121512th Carolina
; COUNTRY: USA
; ZIP: 27627
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/948,564
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Bennett, Virginia C.
; REGISTRATION NUMBER: 37,092
; REFERENCE/DOCKET NUMBER: 5051-409
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-854-1400
; TELEFAX: 919-854-1401
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1831 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 20..1747
; US-08-948-564-15

Query Match      2.3%; Score 45; DB 3; Length 1831;
Best Local Similarity 52.8%; Pred. No. 0.0096;
Matches 121; Conservative 0; Mismatches 105; Indels 3; Gaps 1;

Qy 1008 GATGAGGAGGTACTCGCTCAGATCAGTAACCTGTTATTGCTGGATATGAACCTTCTTCG 1067
Db 1037 GATGCTCAGTTGAGGATGATTTAATGCAATGCTTATTCGGTCTATGAACCAACGCT 1096
Qy 1068 ACAGTCTTGACATGATGTTTACCGACTCTCAGAACAAAGCGGTTCCAGATAAATCTT 1127
Db 1097 GCAGTTCTTACTTGGGAGTCTTCTCTAGCTCAAAATCCTAGCAAAATGAAGAAGCT 1156
Qy 1128 CGAGAAGA--AATTTCAGATCGACACGATATGCTAGCTAGAGAACTTAATGCG 1184
Db 1157 CAACGACAGGTAGATTTGGTGCTGGGTACGGGGAGGCCAATTTTGAATCACTTAAGAA 1216
Qy 1185 TTGCTTATCTCGAAGCGTTTGTAAAGAGTCTCTTCTGTCTAGACCTTC 1233
Db 1217 TTGACATACATTAGATTGTTGTGGAGGCTCTTCGTTTATACCC 1265

RESULT 15
US-09-709-103-3
; Sequence 3, Application US/09709103
; Patent No. 6733991
; GENERAL INFORMATION:
; APPLICANT: Cismoweki, Mary
; APPLICANT: Duzic, Emir
; TITLE OF INVENTION: AGS Proteins and Nucleic Acid Molecules and Uses Therefor
; FILE REFERENCE: 60388-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/709,103
; CURRENT FILING DATE: 2000-11-08
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
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; LENGTH: 1801
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (154)..(996)
; OTHER INFORMATION:
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US-09-709-103-3

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Query Match      2.3%; Score 44.8; DB 3; Length 1801;
Best Local Similarity 95.8%; Pred. No. 0.011;
Matches 46; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 1872 AAAAAAAAAAAAAAAAAAAAAAAAAAGCGCGCTCGAGCCGC 1919
Db 1719 AAAAAAAAAAAAAAAAAAAAAAAAAAGCGCGCTCGAGCATGC 1766
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Search completed: November 21, 2005, 05:06:21  
Job time : 264 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 21, 2005, 16:56:32 ; Search time 7 Seconds  
(without alignments)

89.899 Million cell updates/sec

Title: US-10-066-007A-1

Perfect score: 2852

Sequence: 1 MFILVLTLTGALGAARFASWAS.....RIVGREKEGYQMLQVKPVE 557

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 8323 seqs, 1129788 residues

Total number of hits satisfying chosen parameters: 8323

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:

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2: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*  
5: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*  
7: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*  
8: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	257.5	9.0	509	1	US-10-131-826A-108
2	158	5.5	524	1	US-10-507-106-4
3	150.5	5.3	504	1	US-10-131-826A-64
4	143	5.0	490	1	US-10-507-106-2
5	142	5.0	468	1	US-10-957-569-28
6	86	3.0	643	1	US-10-510-386-8
7	80.5	2.8	450	7	US-11-074-176-212
8	78	2.7	296	7	US-11-074-176-22
9	78	2.7	565	1	US-10-467-962B-109
10	78	2.7	2053	7	US-11-013-759-9
11	77	2.7	799	7	US-11-074-176-348
12	77	2.7	805	7	US-11-074-176-172
13	76.5	2.7	702	1	US-10-510-386-214
14	76.5	2.7	746	7	US-11-074-176-314
15	76.5	2.7	749	7	US-11-074-176-54
16	76	2.7	535	1	US-10-131-826A-124
17	74.5	2.6	756	7	US-11-074-176-202
18	73	2.6	542	7	US-11-074-176-30
19	73	2.6	865	7	US-11-109-156-4
20	73	2.6	1476	1	US-10-647-956A-4
21	72.5	2.5	322	1	US-11-109-156-33
22	72.5	2.5	364	1	US-10-981-873-30
23	72.5	2.5	614	1	US-10-519-447-2
24	72	2.5	242	7	US-11-082-389-366
25	72	2.5	386	7	US-11-022-562-229
					Sequence 108, App
					Sequence 4, Appl
					Sequence 64, Appl
					Sequence 2, Appl
					Sequence 8, Appl
					Sequence 212, App
					Sequence 22, Appl
					Sequence 109, App
					Sequence 9, Appl
					Sequence 348, App
					Sequence 172, App
					Sequence 214, App
					Sequence 314, App
					Sequence 54, Appl
					Sequence 124, App
					Sequence 202, App
					Sequence 30, Appl
					Sequence 4, Appl
					Sequence 33, Appl
					Sequence 30, Appl
					Sequence 2, Appl
					Sequence 366, App
					Sequence 229, App

## ALIGNMENTS

### RESULT 1

US-10-131-826A-108  
; Sequence 108, Application US/10131826A  
; Publication No. US20050245730A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: Deforge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
ACIDS ENCODING THE SAME

FILE REFERENCE: P3330R1C128

CURRENT APPLICATION NUMBER: US/10/131.826A

CURRENT FILING DATE: 2002-04-24

PRIOR APPLICATION NUMBER: 60/049911

PRIOR FILING DATE: 1997-06-18

PRIOR APPLICATION NUMBER: 60/056974

PRIOR FILING DATE: 1997-08-26

PRIOR APPLICATION NUMBER: 60/059113

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059115

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059117

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059122

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059184

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059263

PRIOR FILING DATE: 1997-09-18

PRIOR APPLICATION NUMBER: 60/059352

PRIOR FILING DATE: 1997-09-19

PRIOR APPLICATION NUMBER: 60/059588

PRIOR FILING DATE: 1997-09-19

; Remaining Prior Application data removed - See File wrapper or PALM.

Sequence 5, Appl  
Sequence 4, Appl  
Sequence 7, Appl  
Sequence 8, Appl  
Sequence 37, Appl  
Sequence 248, App  
Sequence 18, Appl  
Sequence 11, Appl  
Sequence 142, App  
Sequence 134, App  
Sequence 90, Appl  
Sequence 6, Appl  
Sequence 73, Appl  
Sequence 10, Appl  
Sequence 318, App  
Sequence 64, Appl  
Sequence 214, App  
Sequence 99, Appl  
Sequence 32, Appl  
Sequence 454, App

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; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 108
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-131-826A-108

Query Match          9.0%; Score 257.5; DB 1; Length 509;
Best Local Similarity 22.0%; Pred. No. 3e-16;
Matches 103; Conservative 94; Mismatches 185; Indels 87; Gaps 18;

QY 66 YREKYGSTRFAGIAGAPVLNSTDPKVFENHVMKEAYDYPKPGMAARVLRATDGVVTAEE 125
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 94 YDPDYAKTL-----LSRDPK-SQYLQK-----FSP-----LLKGLAALD 129
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 126 GEAHKRRHRRIMPSLSAQAVKSMVPIFLEKGMELVDKMMEDAAEKOMAVGESAGEKATR 185
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 130 GPKWFQHRRLTTPGFHNLKAVIEV-----MAHSVMMMLDKWEKICSTQDTS----- 177
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 186 LETEGVDVVDVGRATLDVWALAGFDYKSDSLQNKTNELVY-APVGLTDGFATLDSF-- 242
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 178 -----VEVYEHINSMSLDIIMKCAFSKETNCQTNSTHDPYAKAIFELSKIIFHRLYSLLY 232
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 243 -KAIMWDFVPY---FRMKRHRHEIPTQGLAVRRVGIELMEOKQOAVLGSASDQAVDKK 298
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 233 HSDIIFKLSQGVRFKLSR-----VLNQYDTTIIQERKKSLOAGVKQDNTPKRK 282
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 299 DVQGRDILSLVRANTAANLIPESOKLSDEVLQAIQNLFPAGYETSTVLTWMPHRLSED 358
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 283 ---YQDFLDIV---LSAKDESGSSFSDDIVHSEVSTFLLAGHDTLAAISWILYCLALN 335
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 359 KAVQDKLREICQI--DTPMTDDELNALPYLEAFVKESRLRLOPPSPYANRECLKDEDFI 416
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 336 PEQRCREVRGILDGSSITWDQGENSYTTWCICKETCLRLPAVPSISRD----- 387
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 417 PLAEPVIGRDSVINEVRIKGTWMLPLFNINRSKFIYGEDAEPRPERWLEDVTDLSLN 476
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 388 -LSKPLTFPDGCT-----LPAGITVLSLGLHNNPAVW-KNPKVPDPLRFSSENSDQKH 440
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 477 SIEAPYGHQASFTISGRPRACFGWFAVMAKAFVLTLLRRVQFEPITISHP 525
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 441 ----PYAY-LPFSAGSRNCIGQEFAMIELKVTTIALILLHPRVTPDPTRP 484
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 2
US-10-507-106-4
; Sequence 4, Application US/10507106
; Publication No. US2005024679A1
; GENERAL INFORMATION:
; APPLICANT: Japan Science and Technology Agency
; TITLE OF INVENTION: Gene participating in the synthesis of brassinosteroid
; FILE REFERENCE: 26352U (P503-311PCT)
; CURRENT APPLICATION NUMBER: US/10/507,106
; CURRENT FILING DATE: 2004-09-10
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 4
; LENGTH: 524
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-507-106-4

Query Match          5.5%; Score 158; DB 1; Length 524;
Best Local Similarity 19.7%; Pred. No. 2.8e-07;
Matches 113; Conservative 89; Mismatches 213; Indels 160; Gaps 24;

QY 30 PRESSLY----NLQGP-NHNYFTGNFLDLSA-----RTGEHAKYR 67
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 4 PASAGLFRSPENLFWPYNMDYLVAGFL-VITAGILLRPLWFLRNSKTKDGEEDNE 62
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 68 EK-----YGSTLRF-----AGIAGAPVLNST 88
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 63 EKKKGIMPNGSLGWPVIGETLNFIACGYSSRPVTFMDKRKSLYGVKFKTNIIGTPIIST 122
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 64
; LENGTH: 504
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-131-826A-64

Query Match          5.3%; Score 150.5; DB 1; Length 504;
Best Local Similarity 22.3%; Pred. No. 1.2e-06;
Matches 130; Conservative 78; Mismatches 249; Indels 127; Gaps 25;

Qy 8 TGALGLAAFSWASIAFTSLYLAAPRRSSLYNIQGNHTNYFTGNFLDILSARTGEHAKYR 67
Db 6 TWALLAL--ALLLLLTALSSTRARGHLPPGPTPLP-LILGNLLQLRPGALYSGLMRLS 61
Qy 68 EKYGSTURFAGIAGAPVLNSTDPKVFNVHM-KEAYDYPKPGMAARVLRATGDDGVVTAEG 126
Db 62 KKYGEVFTIYLGPRWPVVVLVQEAAREALGGQAEFPFSGRTVAMLEGTFDGHGVFFSNG 121
Qy 127 EAHKRHRIRIMPSLSAQAVKSMVFIFLEKGMELVDKWMEDAAEKDMAVGESAGSK----- 181
Db 122 ERWQLRKFTMLAL-----RDLGKRGEGBELQAE 152
Qy 182 ----KATRLTEG--VDVKDVGVRATLDVMA--LAG--FDYKSDSLQNKTNELVYAFVGL 231
Db 153 ARCLVEITFGTEGPRFDPSSLQAQTSNVVCSLLFGLRFSYEDKEFQAVVRAAGTLLGV 212
Qy 232 TDGFAPLDSFKAMWDFVPFRTMKRHEIPL-----TQGLAVRRVGIELMEQKQAVL 287
Db 213 SSQGGQTYEMFS--W-----FLRLPGPHKQLLHHVSTLAAFTVRQV-----QHQGNL 259
Qy 288 GSASDAQVDKQVQGRDILSLVRAANIAANLPESQ-----KLSDEVLQAISNLLFAGYET 343
Db 260 -DASGPARD-----LVDAFLKMAQEENQPGTEFTNKMLMTVIYLLFAGTWT 306
Qy 344 SSTVLTMFHRLSDEKAVQDKLRBEICQIDTM-----PTLDELNALPYLEAFVKESLRL 398
Db 307 VSTTVGYTLJJLMKYPHYQKVVREE---LNRELGAQAPSGLDRTRLPYTDVILHEAQL 363
Qy 399 DPPSPYA-NRECLKDEDF---IPLAEPIVGRDGSVINEVRITKGTVMWMLPLFNINRSKP 453
Db 364 LALVPMGIPRTLMRTTRFRGTPLQGTVEVFPLLGSLILHDPNIFK----- 407
Qy 454 IYGEDAEFRFRPRLWLEDVTSLSNSTEAPYHQASFISSGPRACFGWRPAAVEMKAPLFVTL 513
Db 408 ----HPEISLFRDL-DADGRFRKHEA-----FLPFSLGKRVCLGEGKAKELFLFFTTIL 458
Qy 514 RRVQPEPIISHPEYHITLIISRPRIVGREKEGYQMRILQVRPVE 557
Db 459 QAFSLESFPC-PD-----TLSL-KPTVSGLFNIPPAFQLQVRPTD 496

RESULT 4
US-10-507-106-2
; Sequence 2, Application US/10507106
; Publication No. US20050246797A1
; GENERAL INFORMATION:
; APPLICANT: Japan Science and Technology Agency
; TITLE OF INVENTION: Gene participating in the synthesis of brassinosteroid
; FILE REFERENCE: 26352U (PS03-311PCT)
; CURRENT APPLICATION NUMBER: US/10/507,106
; CURRENT FILING DATE: 2004-09-10
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin version 3.1
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; SEQ ID NO 2
; LENGTH: 490
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-507-106-2

Query Match          5.0%; Score 143; DB 1; Length 490;
Best Local Similarity 18.6%; Pred. No. 5.5e-06;
Matches 105; Conservative 94; Mismatches 215; Indels 150; Gaps 21;

Qy 19 ASIAPFSLYL-----APRRSSLYNLQGNHTNYF-----TGNF 51
Db 5 SSSLFTSFPPFIIVIPNKINGLRSSPASKKLNDDHHVTSQSHGPKFPHGSLGWPVIGET 64
Qy 52 LDILSARTGEHAKYREK-----YGSTLRPAGIAGAPVLNSTDPKVFNVHMKAYD----- 102
Db 65 IEFVSSAYSDRPESFMDKRLMYGRVFK-SHIFTATIVSTDAEVNRVAVQSSTAFVPF 123
Qy 103 YPKPGMAARVLRATGCVVTAEGEAHKRHRIM-----IPSLSAQAVKSMVPFLEKGM 157
Db 124 YPK-----TVRELKMGSSILLINGSLHRRPHGLVGLSKPLKQAQIVRDMHK-FLSESM 177
Qy 158 ELVDKWMEDAAEKDMAVGESAGKATRLTEGVDVKDVGVRATLDVNALAGFDY-KSDS 216
Db 178 DLWS-----EDQPVLQDVSKTVAFKVLAKALISVEKGD 212
Qy 217 LQNKTNELVYAFVGLTDGPAFTLDSFKAMWDFVPFRTMKRHEIPLTQGLAVRRVGI 276
Db 213 LEELKREFENFISGL-----MSLPINFPGTQ-LHRSLOAKK 247
Qy 277 ELMEQKQAVLGS-ASDAQVDKQVQGRDILSLVRAANIAANLPESOKLSDEEVLQAQISN 335
Db 248 NMVAKVERIIEGKIRKTKNKEEDDVIKDVVLLK-----DSSEHLTHNLANNMID 300
Qy 336 LLFAGYETSSTVLTMFHRLSDEKAVQDKLRBEICQIDTDMPTLDELN-----AL 385
Db 301 MMIPGHDSVPVLTILAVKFLSDSPAALNLLTKNM-----KLKSLKELTGEPLYWNDYLSL 355
Qy 386 PYLEAFVKESLRLDPPSPYANRECLKDEDFIPLAEPIVGRDGSVINEVRITKGTVMWMLPL 445
Db 356 PLTQKVITETLRMGVNIIGVMRKAMKDVE-----IKGVIPKGCWCFLAYL 400
Qy 446 FNINRSKFIYGEDAEFRFRPRLWLEDVTSLSNSTEAPYHQASFISSGPRACFGWRPAAVEM 505
Db 401 RSVHLDDEAYI-ESPKFNPRWQBE--RDMNTSSFSFPG-----GGORLCPGLDLARLET 451
Qy 506 KAFLEFVTLRRVQF-----EPIISHP 525
Db 452 SVFLHLVTRFRMTAEEDTIINPP 475

RESULT 5
US-10-957-569-28
; Sequence 28, Application US/10957569
; Publication No. US20050246785A1
; GENERAL INFORMATION:
; APPLICANT: COOK, Zhihong et al.
; TITLE OF INVENTION: PROMOTER, PROMOTER CONTROL ELEMENTS, AND COMBINATIONS, AND USES
; FILE REFERENCE: 2750-1577PUS3
; CURRENT APPLICATION NUMBER: US/10/957,569
; CURRENT FILING DATE: 2004-09-30
; PRIOR APPLICATION NUMBER: US 10/950,321
; PRIOR FILING DATE: 2004-09-23
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 28
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-957-569-28

Query Match          5.0%; Score 142; DB 1; Length 468;
```



Db 337 DIYELFGSKDE--IDVSDY--IHKDQG--IVHVGKTTLYDPERFFHTDLKAF--- 388  
 Qy 512 TLRRVQPEPIIHPY--EHTTLISRPRIVRKEGQYQRLQ-----VKPVE 557  
 Db 389 -----QSDIITIGYMHYPNLQKDESI---DLEGYKFTLESIEQGFMRWFIVEPIK 439

RESULT 8  
 US-11-074-176-22  
 ; Sequence 22, Application US/11074176  
 ; Publication No. US20050250135A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Klaenhammer, Todd R.  
 ; APPLICANT: Russell, William M.  
 ; APPLICANT: Altermann, Eric  
 ; APPLICANT: McAuliffe, Olivia  
 ; APPLICANT: Perill, Andrea Azcarate  
 ; TITLE OF INVENTION: Nucleic Acid Sequences Encoding  
 ; TITLE OF INVENTION: Stress-Related Proteins and Uses Therefore  
 ; FILE REFERENCE: 5051-694  
 ; CURRENT APPLICATION NUMBER: US/11/074,176  
 ; CURRENT FILING DATE: 2005-03-07  
 ; PRIOR APPLICATION NUMBER: 60/551,161  
 ; PRIOR FILING DATE: 2004-03-08  
 ; NUMBER OF SEQ ID NOS: 381  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 22  
 ; LENGTH: 296  
 ; TYPE: PRT  
 ; ORGANISM: Lactobacillus acidophilus  
 US-11-074-176-22

Query Match 2.7%; Score 78; DB 7; Length 296;  
 Best Local Similarity 26.8%; Pred. No. 1.7;  
 Matches 57; Conservative 23; Mismatches 69; Indels 64; Gaps 13;  
 Qy 113 LRIATGCVVTAEG---FAHKHRRIMIPSLSAQAVKSMVFLEKGMELVDKWMED--- 166  
 Db 15 LRLLT---ITAKGVVSAQKRDH--LWSASSAVLGRTLVGLSLLAGAEITDK--EELTV 66  
 Qy 167 -----AAEKDMVAGESAGEKKATRL-----ETEGVDVKVWVGGRATLDVMA 208  
 Db 67 RLLGNPVGPAIVTADLVK---KGYVKNPHIALPPKENGHIDVKVAGQGFVETKDL 123  
 Qy 209 GFDYKSDSLQKNTNELYVAFVGLTDFGAPTLDSFKAIMWDFVFPRTMKRHEIPLTQGL 268  
 Db 124 GL-----KEPYTGQVPVSG-----EIAEDFAYY---LTKSEQIPSAVGL 160  
 Qy 269 AV-----SRRVGHELMQKQAVLGSASDAQVDK 297  
 Db 161 SVFVNPNSIG-EAGGFMLQALPG-ASDALIDK 191

RESULT 9  
 US-10-467-962B-109  
 ; Sequence 109, Application US/10467962B  
 ; Publication No. US20050246784A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Plesch, Gunnar  
 ; APPLICANT: Blau, Astrid  
 ; APPLICANT: Daeschner, Klaus  
 ; APPLICANT: Klein, Mathieu  
 ; TITLE OF INVENTION: Identification of Herbicidally Active Substances  
 ; FILE REFERENCE: 2000 857  
 ; CURRENT APPLICATION NUMBER: US/10/467,962B  
 ; CURRENT FILING DATE: 2003-08-14  
 ; PRIOR APPLICATION NUMBER: PCT/EP02/01466  
 ; PRIOR FILING DATE: 2002-02-13  
 ; NUMBER OF SEQ ID NOS: 109  
 ; SOFTWARE: PatentIn Vers. 2.0  
 ; SEQ ID NO 109  
 ; LENGTH: 565  
 ; TYPE: PRT

; ORGANISM: Arabidopsis thaliana  
 US-10-467-962B-109  
 Query Match 2.7%; Score 78; DB 1; Length 565;  
 Best Local Similarity 16.0%; Pred. No. 4.7;  
 Matches 56; Conservative 59; Mismatches 92; Indels 144; Gaps 17;  
 Qy 176 ESAGEKKATRL--ETEGVDVKD-----WVGRATLDVMAAL--FDYKS--DSLQKNTNE 223  
 Db 273 KACSEKALRFGQVHSLVVRMIKTDVFGTSLMDMYAKGGEISDCRKFVDFGNSRNTV 332  
 Qy 224 LYVAFVG--LTDGFAPTLDSFKAIMWDFVFPRTMKRHEIPLTQGLAVARRVGIEMEQ 281  
 Db 333 TWTSIIAAHAREGFGE-----EASLFRIMKRH-----LIANNLTVELHAQ 374  
 Qy 282 KQAVLGSASDAQVDKQVQGRDILSLVPRANTANLPEKQKLSDEEVLQIAISLLPAGY 341  
 Db 375 -----IIKNSIEKN-----VYIG- 387  
 Qy 342 ETSSTVLTWTFHRLSEDKAVQDKLREICQIDTDMPTLD-----ELNAL 385  
 Db 388 ----STLVWLYCKGSGSDAFNVLQ-----LPSRDVSVWTAMISGCSLGHSEAL 435  
 Qy 386 PYLEAFVKESLRLDPPSPY----ANRECLKDEDFIPLAEPVIGRD-----GSVINEVR 434  
 Db 436 DFLKEMIQEGVE---PNPFTYSSALKACANSESL-----IGRSIHSIAKKNHLSNVF 486  
 Qy 435 ITKGTVMVLPFNI-----NRSKFIYGEDAEFRPRWL 468  
 Db 487 VGSALIHIMPEKNLVSWKAMIMGYARNGFCREALKLMYRMEAGEFVEDDYI 537

RESULT 10  
 US-11-013-759-9  
 ; Sequence 9, Application US/11013759  
 ; Publication No. US20050249747A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Loosmore, Sheena M.  
 ; APPLICANT: Sasaki, Ken  
 ; APPLICANT: Yang, Yan Ping  
 ; APPLICANT: Klein, Michel H.  
 ; TITLE OF INVENTION: RECOMBINANT HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE  
 ; FILE REFERENCE: 1038-921MIS:1b  
 ; CURRENT APPLICATION NUMBER: US/11/013,759  
 ; CURRENT FILING DATE: 2004-12-16  
 ; PRIOR APPLICATION NUMBER: US/09/361,619  
 ; PRIOR FILING DATE: 1999-07-27  
 ; NUMBER OF SEQ ID NOS: 32  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 9  
 ; LENGTH: 2053  
 ; TYPE: PRT  
 ; ORGANISM: Moraxella catarrhalis  
 US-11-013-759-9

Query Match 2.7%; Score 78; DB 7; Length 2053;  
 Best Local Similarity 19.4%; Pred. No. 36;  
 Matches 71; Conservative 73; Mismatches 138; Indels 84; Gaps 18;  
 Qy 32 RSSLYNLQGNHTNYFT-GNFDILSARTGBEHAKYREKYGSTLRFAGIAGAPVLN---- 86  
 Db 664 KTKLNSNGTSGNKKFSVSNADNNSLVTAQDLADLYLNKVNETAADSA-LPSFKVQNGDNS 722  
 Qy 87 -----STDPKVFNHVMKEAYDYPKPGMAARVLRATG-----DGVVTAE---G 126  
 Db 723 NNATVVGKDTNGKTFNTLLKKG---ENGVNITNR-ATGTVTFQIDQSNGLTTPKLTVG 777  
 Qy 127 EAHKHEHRIM--IPSLSAQAVKSMVPIFLEKGMELVDKWMEDAAEKDMVAGESAGEKKAT 184  
 Db 778 SDTNGRLVIEQVPSADGNSTKNII-----KGLSTPLSPSIASPSGRNLTALGNT----- 825  
 Qy 185 RLETEGVVDKQWVGGRATLDVMAALAGFDYKSDSLQKNTNELYVAFVGLTDFGAPTLDSFKA 244

```
Db      826  -----IEEKDKSNASIDDVLNAGFNKNGKDFVSTYDT- VDFIDGNATT-----AT 874
Qy      245  IMWDFVYPTMKRRRHEIPTQ-----GLAVRRRVGIELMEOKQAVLGSDAQAVDKK 298
Db      875  VTYDEAN--QTSKVAVDVNDTEIETLTDGNGKKQLGVKTIKLTETSTNGNATTFSTD-- 930
Qy      299  DVQGRDILSLVRANTAANLPESOKLSDEEVLAQISNLLFAGYETSSVTL-TWMFHRLSE 357
Db      931  -----DDHALVKASDIAGNL---NTLAE-----IHTTKGTANTALQFTVKKVDE 973
Qy      358  DKAVQD 363
Db      974  NDKADD 979

RESULT 11
US-11-074-176-348
; Sequence 348, Application US/11074176
; Publication No. US20050250135A1
; GENERAL INFORMATION:
; APPLICANT: Klaenhammer, Todd R.
; APPLICANT: Russell, William M.
; APPLICANT: Altermann, Eric
; APPLICANT: McAuliffe, Olivia
; APPLICANT: Peril, Andrea Azcarate
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding
; FILE REFERENCE: 5051-694
; CURRENT APPLICATION NUMBER: US/11/074,176
; PRIOR FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: 60/551,161
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 348
; LENGTH: 799
; TYPE: PRT
; ORGANISM: Lactobacillus acidophilus
US-11-074-176-348

Query Match      2.7%; Score 77; DB 7; Length 799;
Best Local Similarity 21.3%; Pred. No. 10;
Matches 94; Conservative 72; Mismatches 169; Indels 106; Gaps 24;

Qy 123 TAEGEAH-----KRHRIMIPSLSAQAVKSMVPIFLEKGMELVD--KMEDAAEK 170
Db 360 TAGDQRMAMPITNGGDKPKRLNLPYRNFAKFDKPGSV--AQDMVEWAKYLNEVAKL 418
Qy 171 DMV--GESAGEKATRLTEGVVK--DW---VGRATLDVNALAGFDYKSDSLQNKTNEL 224
Db 419 NPTTFRGFGPDESKNSRLFLKLLDDQKQWEPVEHPENDENLAPSGRVIDSOLSEHQDEGF 478
Qy 225 YVAFVGLT--DGFAPTLDSF-----KALMWDVPVYFTMKR---RHEIPLTOGLAVS--- 271
Db 479 LEGYV-LTGRHGFPATYEAFGRVVDVSMLTQHMKWLKAKEQYWRHDPYSLNFVATSTVPQ 537
Qy 272 -----RRVGI--ELMEQKQAVLGS--ASDQ-----AVDKQDVQGRDILSLVRANTA 315
Db 538 QDHNGYTHODPGILTHLYEKNRPDVLVHEYLPSDTNTLLAVGNKAFTRDRCINVLVTSKQP 597
Qy 316 A----NLPESOKLSDEEVLAQIS-----NLLFAGYETSSVTLTWMFHRLSEDKAV 361
Db 598 RPQWFSIEEAQKLVKDG--LSYIDWASTDKGVKPDIVFASTEPTETIETLAAIDILHDKFP 656
Qy 362 QDKLREICQIDTDMPTLDENALPYLEAFVKESLRDPPSPYANRECLKDEDFIPLAEP 421
Db 657 DLKIR-----YINVIDVKLM-----SPKDNKNGISDEEF-----DR 688
Qy 422 VIGRDSGVINEVRITKGTWMLPLFNIRSK-----FIYGDAEEFRP-----ERWLE 469
Db 689 LFPKDVPIFAWHGYKSMMESI-WFARNRHNHVIHCYEENGDIITTFDMRVNLHLDRF-D 746
```

```
Qy      470  DVTDSLNSIEAPYCHQASFIS 490
Db      747  LAKDAVESVDKLKGKNADFIS 767

RESULT 12
US-11-074-176-172
; Sequence 172, Application US/11074176
; Publication No. US20050250135A1
; GENERAL INFORMATION:
; APPLICANT: Klaenhammer, Todd R.
; APPLICANT: Russell, William M.
; APPLICANT: Altermann, Eric
; APPLICANT: McAuliffe, Olivia
; APPLICANT: Peril, Andrea Azcarate
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding
; FILE REFERENCE: 5051-694
; CURRENT APPLICATION NUMBER: US/11/074,176
; PRIOR FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: 60/551,161
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 172
; LENGTH: 805
; TYPE: PRT
; ORGANISM: Lactobacillus acidophilus
US-11-074-176-172

Query Match      2.7%; Score 77; DB 7; Length 805;
Best Local Similarity 21.3%; Pred. No. 10;
Matches 94; Conservative 72; Mismatches 169; Indels 106; Gaps 24;

Qy 123 TAEGEAH-----KRHRIMIPSLSAQAVKSMVPIFLEKGMELVD--KMEDAAEK 170
Db 366 TAGDQRMAMPITNGGDKPKRLNLPYRNFAKFDKPGSV--AQDMVEWAKYLNEVAKL 424
Qy 171 DMV--GESAGEKATRLTEGVVK--DW---VGRATLDVNALAGFDYKSDSLQNKTNEL 224
Db 425 NPTTFRGFGPDESKNSRLFLKLLDDQKQWEPVEHPENDENLAPSGRVIDSOLSEHQDEGF 484
Qy 225 YVAFVGLT--DGFAPTLDSF-----KALMWDVPVYFTMKR---RHEIPLTOGLAVS--- 271
Db 485 LEGYV-LTGRHGFPATYEAFGRVVDVSMLTQHMKWLKAKEQYWRHDPYSLNFVATSTVPQ 543
Qy 272 -----RRVGI--ELMEQKQAVLGS--ASDQ-----AVDKQDVQGRDILSLVRANIA 315
Db 544 QDHNGYTHODPGILTHLYEKNRPDVLVHEYLPSDTNTLLAVGNKAFTRDRCINVLVTSKQP 603
Qy 316 A----NLPESOKLSDEEVLAQIS-----NLLFAGYETSSVTLTWMFHRLSEDKAV 361
Db 604 RPQWFSIEEAQKLVKDG--LSYIDWASTDKGVKPDIVFASTEPTETIETLAAIDILHDKFP 662
Qy 362 QDKLREICQIDTDMPTLDENALPYLEAFVKESLRDPPSPYANRECLKDEDFIPLAEP 421
Db 663 DLKIR-----YINVIDVKLM-----SPKDNKNGISDEEF-----DR 694
Qy 422 VIGRDSGVINEVRITKGTWMLPLFNIRSK-----FIYGDAEEFRP-----ERWLE 469
Db 695 LFPKDVPIFAWHGYKSMMESI-WFARNRHNHVIHCYEENGDIITTFDMRVNLHLDRF-D 752
Qy 470  DVTDSLNSIEAPYCHQASFIS 490
Db      753  LAKDAVESVDKLKGKNADFIS 773

RESULT 13
US-10-510-386-214
; Sequence 214, Application US/10510386
; Publication No. US2005024492A1
; GENERAL INFORMATION:
; APPLICANT: Andersen, Jens Tonne
```

Query Match 2.7%; Score 76.5; DB 7; Length 746;  
Best Local Similarity 19.6%; Pred. No. 10;  
Matches 96; Conservative 76; Mismatches 175; Indels 143; Gaps 25;



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OM protein - protein search, using sw model

Run on: November 21, 2005, 16:56:42 ; Search time 166 Seconds  
(without alignments)

1401.994 Million cell updates/sec

Title: US-10-066-007A-1

Perfect score: 2852

Sequence: 1 MFILVLLTGALGLAASFWSAS.....RIVGREKGYQMRLQVLPVE 557

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA\_Main.\*

1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*

2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*

3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*

4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*

5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*

6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2852	100.0	557	4	US-10-066-007-1
2	2852	100.0	557	4	US-10-066-007-3
3	419	14.7	595	5	US-10-751-235-33
4	399	14.0	504	5	US-10-804-772-24
5	398.5	14.0	503	4	US-10-313-963A-56
6	396.5	13.9	503	4	US-10-146-575-2
7	396.5	13.9	503	5	US-10-745-237-408
8	395.5	13.9	503	5	US-10-732-923-1079
9	394	13.8	485	5	US-10-690-991-2
10	394	13.8	485	5	US-10-833-296-2
11	394	13.8	485	5	US-10-516-338-8
12	394	13.8	485	6	US-11-076-967-2
13	392.5	13.8	543	4	US-10-425-115-294241
14	387.5	13.6	508	5	US-10-751-235-35
15	387	13.6	517	4	US-10-437-963-110700
16	387	13.6	523	4	US-10-437-963-157051
17	385.5	13.5	503	3	US-09-957-997-3
18	385	13.5	502	5	US-10-631-467-847
19	384.5	13.5	425	5	US-10-751-235-36
20	384.5	13.5	513	4	US-10-686-947-272
21	384.5	13.5	513	5	US-10-943-507-267
22	384.5	13.5	650	4	US-10-437-963-164419
23	384	13.5	537	4	US-10-425-114-38180
24	382	13.4	526	4	US-10-425-115-360975
25	381.5	13.4	527	4	US-10-425-115-233616
26	381	13.4	520	4	US-10-437-963-189675
27	380	13.3	529	4	US-10-425-115-209345

28	377.5	13.2	523	4	US-10-425-115-191779	Sequence 191779,
29	377.5	13.2	527	4	US-10-425-114-67055	Sequence 67055, A
30	377.5	13.2	579	5	US-10-751-235-38	Sequence 38, Appl
31	376.5	13.2	547	4	US-10-425-114-65616	Sequence 65616, A
32	374.5	13.1	461	4	US-10-686-947-176	Sequence 176, App
33	374.5	13.1	461	5	US-10-943-507-174	Sequence 224659,
34	372.5	13.1	528	4	US-10-425-115-224659	Sequence 169524,
35	371	13.0	516	4	US-10-437-963-169524	Sequence 216, App
36	370	13.0	521	4	US-10-686-947-216	Sequence 213, App
37	370	13.0	521	5	US-10-943-507-213	Sequence 184472, A
38	368.5	12.9	523	4	US-10-437-963-184472	Sequence 61218, A
39	368.5	12.9	547	4	US-10-425-114-61218	Sequence 59349, A
40	368.5	12.9	560	4	US-10-425-114-59349	Sequence 59350, A
41	368.5	12.9	562	4	US-10-425-114-59350	Sequence 2, Appl1
42	367	12.9	520	3	US-09-932-901-2	Sequence 264, App
43	367	12.9	521	4	US-10-686-947-264	Sequence 259, App
44	367	12.9	521	5	US-10-943-507-259	Sequence 174346,
45	367	12.9	525	4	US-10-437-963-174346	

## ALIGNMENTS

### RESULT 1

US-10-066-007-1

; Sequence 1, Application US/10066007

; Publication No. US20030077691A1

; GENERAL INFORMATION:

; APPLICANT: HOSHINO, Tatsuo

; APPLICANT: OJIMA, Kazuyuki

; APPLICANT: SETOGUCHI, Yutaka

; TITLE OF INVENTION: ASTAXANTHIN SYNTHETASE

; FILE REFERENCE: ASTAXANTHIN SYNTHETASE

; CURRENT APPLICATION NUMBER: US/10/066,007

; PRIOR FILING DATE: 2001-02-01

; PRIOR APPLICATION NUMBER: US/09/518,386

; PRIOR FILING DATE: 2000-03-03

; PRIOR APPLICATION NUMBER: EP 99104668.1

; PRIOR FILING DATE: 1999-03-09

; PRIOR APPLICATION NUMBER: EP 00101666.6

; PRIOR FILING DATE: 2000-02-01

; NUMBER OF SEQ ID NOS: 32

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1

; LENGTH: 557

; TYPE: PRT

; ORGANISM: Phaffia rhodozyma

; FEATURE:

; NAME/KEY: TRANSIT

; LOCATION: (1)..(26)

; US-10-066-007-1

Query Match 100.0%; Score 2852; DB 4; Length 557;  
Best Local Similarity 100.0%; Pred. No. 5.2e+231;  
Matches 557; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MFILVLLTGALGLAASFWSASIAFFSLYLAPRRSSLYNLQGNHTNYFTGNFLDLSARTG	60
DB	1	MFILVLLTGALGLAASFWSASIAFFSLYLAPRRSSLYNLQGNHTNYFTGNFLDLSARTG	60
QY	61	EEHAKYREKYGSTLRFAGIAGAPVLNSTDPKVFNVHVKMEAYDYPKPGMAARVLRLATGDG	120
DB	61	EEHAKYREKYGSTLRFAGIAGAPVLNSTDPKVFNVHVKMEAYDYPKPGMAARVLRLATGDG	120
QY	121	VVTAGEAHKRRHRRIMIPSLSAQAVKSMVPFLEKGMELVDKMMEDAAEKMAVGESAGE	180
DB	121	VVTAGEAHKRRHRRIMIPSLSAQAVKSMVPFLEKGMELVDKMMEDAAEKMAVGESAGE	180
QY	181	KKATRLTEGVDDVQVGRATLDVNALAGFDYKSDSLQNKTNELVYAFVGLTDGFAPTLD	240
DB	181	KKATRLTEGVDDVQVGRATLDVNALAGFDYKSDSLQNKTNELVYAFVGLTDGFAPTLD	240
QY	241	SFKATMWDVPVFRFTMKRRHEIPLTQGLAVSRVRVIELMEQKKQAVLGSASDAQVDKDDV	300

[illegible]

```

RESULT 2
US-10-066-007-3
; Sequence 3, Application US/10066007
; Publication No. US20030077691A1
; GENERAL INFORMATION:
; APPLICANT: HOSHINO, Tatsuo
; APPLICANT: OJIMA, Kazuyuki
; APPLICANT: SETOGUCHI, Yutaka
; TITLE OF INVENTION: ASTAXANTHIN SYNTHETASE
; FILE REFERENCE: ASTAXANTHIN SYNTHETASE
; CURRENT APPLICATION NUMBER: US/10/066,007
; CURRENT FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: US/09/518,386
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: EP 99104668.1
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: EP 00101666.6
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 557
; TYPE: PRT
; ORGANISM: Phaffia rhodozyma
US-10-066-007-3

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Qy 301 QGRDILSLVRANTAANLPESQKLSDEEVLQAQISNLLFAGYETSSVTLTWMPHRLSEDKA 360
Db 301 QGRDILSLVRANTAANLPESQKLSDEEVLQAQISNLLFAGYETSSVTLTWMPHRLSEDKA 360
Qy 361 VQDKLREIEICQIDTMDPTLDELNALPYLEAFVKESLRLDPPSPYANRECLKDQEDFIPLAE 420
Db 361 VQDKLREIEICQIDTMDPTLDELNALPYLEAFVKESLRLDPPSPYANRECLKDQEDFIPLAE 420
Qy 421 PVIGRDSGVINEVRITKGTVMWMLPLFNINRSKFYIGEDAEFPFRPWLEDBVTDLSNSIEA 480
Db 421 PVIGRDSGVINEVRITKGTVMWMLPLFNINRSKFYIGEDAEFPFRPWLEDBVTDLSNSIEA 480
Qy 481 PYGHOAQSFISGPRACFCGWRFAVAEMKAEFLVTLRRVQPEPIISHPEYEHITLIISRPRIV 540
Db 481 PYGHOAQSFISGPRACFCGWRFAVAEMKAEFLVTLRRVQPEPIISHPEYEHITLIISRPRIV 540
Qy 541 GREKEGYQMRLQVAPVE 557
Db 541 GREKEGYQMRLQVAPVE 557

RESULT 3
US-10-751-235-33
; Sequence 33, Application US/10751235
; Publication No. US20050150002A1
; GENERAL INFORMATION:
; APPLICANT: Dellapenna, Dean
; APPLICANT: Tian, Li
; APPLICANT: Kim, Joonyul
; TITLE OF INVENTION: Novel Carotenoid Hydroxylases for Use in Engineering Carotenoid
; TITLE OF INVENTION: Metabolism in Plants
; FILE REFERENCE: MSU-08604
; CURRENT APPLICATION NUMBER: US/10/751,235
; CURRENT FILING DATE: 2004-01-02
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 33
; LENGTH: 595
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-751-235-33

```

	Query Match	100.0%;	Score 2852;	DB 4;	Length 557;
	Best Local Similarity	100.0%;	Pred. No. 5.2e-231;		
	Matches 557;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0
Qy	1	MFILVLLTGALGAAFSWASIAFFSLYLAPRRSSLYNLQGNPHNYETGNFLDILSARTG	60		
Db	1	MFILVLLTGALGAAFSWASIAFFSLYLAPRRSSLYNLQGNPHNYETGNFLDILSARTG	60		
Qy	61	EBHAKYREKYGSTLRPAGIAGAPVUNSTDPKVFNNHVKMEAYDPKPGMAARVLRIATGDG	120		
Db	61	EBHAKYREKYGSTLRPAGIAGAPVUNSTDPKVFNNHVKMEAYDPKPGMAARVLRIATGDG	120		
Qy	121	VVTAGEAHHKRHRRIWIPSLSAQAVKSMVPFIPEKGMELVDKWMDEAAEKDMAVGESAGE	180		
Db	121	VVTAGEAHHKRHRRIWIPSLSAQAVKSMVPFIPEKGMELVDKWMDEAAEKDMAVGESAGE	180		
Qy	181	KKATRLTEGVVDVKDWGREATLDVVALAGFPDYKSDSLQNKNTNELYVAFGLTGGPAPTLTD	240		
Db	181	KKATRLTEGVVDVKDWGREATLDVVALAGFPDYKSDSLQNKNTNELYVAFGLTGGPAPTLTD	240		
Qy	241	SPKAIWMDVPVYFRYTKRRRHEIPLTQGLAVSRRRVGIELMEOKQAVLGASDAQVADKKDV	300		
Db	241	SPKAIWMDVPVYFRYTKRRRHEIPLTQGLAVSRRRVGIELMEOKQAVLGASDAQVADKKDV	300		



Db 415 PPTQDMKKLYTTRVNNESRLYPQPVLIIRSI-----DNDILGEYPI 459  
Qy 436 TKGTMVLMPLFNINRSFIYGEDAEPRPRERWLEDVTD-----SLSNTEAPYGHQASFISSG 491  
Db 460 KRGEIDIFISVNLHRSP-LHWDDAEKENPERWPLDGNPNETNQNFSLYPFG-----GG 512  
Qy 492 PRACFGHRRFAVAEMKAFLVTLRRVQFE 519  
Db 513 PRKICGDMFASFENVVAIAMLIRRFNFQ 540

RESULT 4  
US-10-804-772-24  
; Sequence 24, Application US/10804772  
; Publication No. US20040244077A1  
; GENERAL INFORMATION:  
; APPLICANT: Azpiroz, Ricardo  
; APPLICANT: Choe, Sungchwa  
; APPLICANT: Feldmann, Kenneth A.  
; TITLE OF INVENTION: DMF4 POLYNUCLEOTIDES, POLYPEPTIDES AND USES THEREOF  
; FILE REFERENCE: 11696-070001  
; CURRENT APPLICATION NUMBER: US/10/804,772  
; PRIOR FILING DATE: 2004-03-18  
; PRIOR APPLICATION NUMBER: US/09/502,426  
; PRIOR FILING DATE: 2000-02-11  
; PRIOR APPLICATION NUMBER: US 60/119,657  
; PRIOR FILING DATE: 1999-02-11  
; PRIOR APPLICATION NUMBER: US 60/119,658  
; PRIOR FILING DATE: 1999-02-11  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 24  
; LENGTH: 504  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-804-772-24

Query Match 14.0%; Score 399; DB 5; Length 504;  
Best Local Similarity 28.4%; Pred. No. 1.5e-24;  
Matches 156; Conservative 83; Mismatches 182; Indels 128; Gaps 24;  
Qy 13 LAAPSW--ASTAFFSLYLAPRRS--SLYNLQG--PNHTNY--FTGNFLDILSARTG-----E 61  
Db 7 LAMETWLLAVSLVLLYLYGTHSHGLFKKLGIPGTPLPFLGN---ILSYHKGFCMPDME 63  
Qy 62 EHAKYREKYGSLRFAGIAGAPVLNSTDPKVFNNHYM--KEAYD-----YKPGMAARVL 113  
Db 64 CHKYKGVWGF---YDG--QQPVLAITDPMIKLVKKECYSVFTNRPPFGVGPMSAI 118  
Qy 114 RIATGDGVVTAAGEAHKRRIMIPSLSAQAVKSVPIFLEKGMELVDKMDAEDAAEKDWA 173  
Db 119 SI-----ABDEEWKRLRLSLLPTFTSGKLKENVPITIAQYGDVLRNLRRE----- 163  
Qy 174 VESAGEKATLETGEGVDVVDKMGVGRATLDVMALAGEDYKSDSLQNKTNELYNLVAFVGLTD 233  
Db 164 -----RETGKPVTLKDVFGAYSMVDVITSSSGVNVDSLNNPD----- 201  
Qy 234 GFAPTLDSFKAIM--WDFV--PYFRITMK--RRHEIPLTQGL-----AVSRVVG 275  
Db 202 ---PLVENTKLLRFDLPDFLPPFLSIIVPPFLIPILEVLNICVFPREVTNFLRKAVRME 258  
Qy 276 IELMOKQAVLGASDQAVKDVQGVGRDILSLVRANITANLPSQK--LSDEEVLAQIS 334  
Db 259 SRLDQTQHRV-----DFLOLMIDSHKNSKETESHKALSDELVAQSI 301  
Qy 335 NLLFAGYETSSVLTWTFHRLSEDKAVQDKLREEICQI---DTDMPTLDELNALPYLEAFV 392  
Db 302 IFIFAGYETSSVLSFIMYELATHPDVQKQEEIDAVLPNKAPPTVDTVLOMVELDWV 361  
Qy 393 KESLRDPPSPYANRECLDEDFIPLAEPVIGRDSGVINEVRITKGTWVMLPLFNINRSK 452  
Db 362 NETLRLFPFAMRLERVKCKDVE-----INGMFI PKGVVVMIPSYALHRDP 406

Qy 453 FIYGEDAEPRPRERWLEDVTDLSNS-TEAPYGHQASFISSGPRACFGHRRFAVAEMKAFLV 511  
Db 407 -KWTPEPEKFLPERFSKONKNDIPYIYTPFG-----SGPRNCIGMRFALMNMKLALIR 459  
Qy 512 TLRRVQFEP 520  
Db 460 VLQNFSPKP 468  
RESULT 5  
US-10-313-963A-56  
; Sequence 56, Application US/10313963A  
; Publication No. US2004002078A1  
; GENERAL INFORMATION:  
; APPLICANT: Boutell, Jonathan  
; APPLICANT: Godber, Benjamin  
; APPLICANT: Hart, Darren  
; APPLICANT: Blackburn, Jonathan  
; TITLE OF INVENTION: Arrays  
; FILE REFERENCE: KIL-001  
; CURRENT APPLICATION NUMBER: US/10/313,963A  
; CURRENT FILING DATE: 2003-06-19  
; PRIOR APPLICATION NUMBER: US 60/335,806  
; PRIOR FILING DATE: 2001-12-05  
; PRIOR APPLICATION NUMBER: US 60/410,815  
; PRIOR FILING DATE: 2002-09-16  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 56  
; LENGTH: 503  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-313-963A-56

Query Match 14.0%; Score 398.5; DB 4; Length 503;  
Best Local Similarity 28.7%; Pred. No. 1.7e-24;  
Matches 153; Conservative 88; Mismatches 195; Indels 97; Gaps 24;  
Qy 13 LAAPSW--ASTAFFSLYLAPRRS--SLYNLQG--PNHTNY--FTGNFLDILSARTG-----E 61  
Db 7 LAMETWLLAVSLVLLYLYGTHSHGLFKKLGIPGTPLPFLGN---ILSYHKGFCMPDME 63  
Qy 62 EHAKYREKYGSLRFAGIAGAPVLNSTDPKVFNNHYM--KEAYD---PKPGMAARVLRIAT 117  
Db 64 CHKYKGVWGF---YDG--QQPVLAITDPMIKLVKKECYSVFTNRPPFGVGPMSA- 117  
Qy 118 GDGVVTAAGEAHKRRIMIPSLSAQAVKSVPIFLEKGMELVDKMDAEDAAEKDVAECES 177  
Db 118 ---ISIAEDEEWKRLRLSLLPTFTSGKLKENVPITIAQYGDVLRNLRREA----- 164  
Qy 178 AGEKATLET-EGVDVVDKMGVGRATLDVMALAGDYKSDSLQNKTNELYNLVAFVGLTDCFA 236  
Db 165 -----ETGKPVTLKDVFGAYSMVDVITSSSGVNVDSLNNPD----- 201  
Qy 237 PTLDSFKAIM--WDFV--PYFRITMK--RRHEIPLTQGLAV---SRRVGIELMEOKQAVLGSA 290  
Db 202 PFVENTKLLRFDLPDFLPPFLSIIVPPFLIPILEVLNICVFPREVTNFLRKSVK- ---M 256  
Qy 291 SDQAVDKDVQGVGRDILSLVRANITANLPSQKLSDEEVLAQISNLLFAGYETSSVLTW 350  
Db 257 KESRLDQTQHRVDFLQMLIDSONSKETESHKALSDELVAQSIIFIFAGYETSSVLSF 316  
Qy 351 MFHRLSEDKAVQDKLREEICQI---DTDMPTLDELNALPYLEAFVKESLRLDPPSPYANRE 408  
Db 317 IMYELATHPDVQKQEEIDAVLPNKAPPTVDTVLOMVELDWVNETLRLFPFAMRLERV 376  
Qy 409 CLKDEDFIPLAEPVIGRDSGVINEVRITKGTWVMLPLFNINRSKFIYGEDAEPRERWL 468  
Db 377 CKKQVE-----INGMFI PKGVVVMIPSYALHRDP--KYWTEPEKFLPERFS 420  
Qy 469 EDVTDLSNS-TEAPYGHQASFISSGPRACFGHRRFAVAEMKAFLVTLRRVQFEP 520  
Db 421 KKNKNDIPYIYTPFG-----SGPRNCIGMRFALMNMKLALIRVLQNFSPKP 467

```

; APPLICANT: Midgley, Carol
; TITLE OF INVENTION: Cell Cycle Progression Proteins
; FILE REFERENCE: P0158190 CYK
; CURRENT APPLICATION NUMBER: US/10/745,237
; CURRENT FILING DATE: 2003-12-23
; PRIOR APPLICATION NUMBER: US 60/439,123
; PRIOR FILING DATE: 2003-01-10
; PRIOR APPLICATION NUMBER: US 60/468,402
; PRIOR FILING DATE: 2003-05-06
; NUMBER OF SEQ ID NOS: 600
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 408
; LENGTH: 503
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: P08684
US-10-745-237-408

Query Match      13.9%; Score 396.5; DB 5; Length 503;
Best Local Similarity 28.7%; Pred. No. 2.5e-24;
Matches 153; Conservative 88; Mismatches 195; Indels 97; Gaps 24;

QY 13 LAAFSW--ASIAFFSLYLAPRRS--SLYNLQ--PNHTNY--FTGNFLDILSARTG-----E 61
Db 7 LAMETWLLAVSLVLLYLYGTHSHGLFKGLGIPGTPLPFLGN---ILSYHKGFCMFDM 63
QY 62 EHAKYREKYGSTLRFAGIAGAPVLNSTDPKVFNHVM--KEAYDY---PKPGMAARVLRIAT 117
Db 64 CHKKGKVGWGF---YDG--QQPVLAITDPMIKTVLVKECVSVFTNRRPFGVGMKSA- 117
QY 118 GGVVTAEGEAHKHRRIMIPSLSAQAVKSMVPIFLEKGMELVDKMDAEDAKDMVAGES 177
Db 118 ---ISIADEEWRKLSLSPTFTSGKLKEMVPIIAQYGDVLVRLNREA----- 164
QY 178 AGEKKATRLT--EGVDVKDWVGRATLDVMALAGFDYKSDSLQNKTNELYVAFVGLTDGFA 236
Db 165 -----ETGKPVTLKDVFGAYSMDVITSTSGVNIIDSLNNPD----- 201
QY 237 PTLDSFKAIM-WDFV-PYFRTMK--RRHEIPLTQGLAV---SRRVGIELMEQKQAVLGSA 290
Db 202 PFVENTKLLRFDLDPFPLSITVPFPLIPILEVNLICVFPREVTFNLRKSVKR-----M 256
QY 291 SDQAVDKDQVGRDILSLVRANIAANLPESQKLSDEEVLQAISNLLFAGYETSSTVLTW 350
Db 257 KESRLDQTKHRVDFQLMIDSONSKETESHKALSDELVAQSIIPIFAGYETTSVLSF 316
QY 351 MFHRLSEDKAVQDKLREEICQI--DTPMTLDLDELNALPYLEAFVKESLRDPPSPYANRE 408
Db 317 IMVELATHPDVQOKLQEEIDAVLNPKAPPTYDVTVLQMEYLDVMVNETLRFPIAMRLERV 376
QY 409 CLKDEDFIPLAEPVIGRGSVINEVRITKGTWMLPLFNINRSKFIYGEAEFRPRERWL 468
Db 377 CKKQVE-----INGMFIPKGVWVWIPSYALHRDP-KYWTPEKFLPERFS 420
QY 469 EDVTDLSNS-IEAPYGHQASFIQPRACFGWRFAVAEMKAFLVFTLRRVQFEP 520
Db 421 KKNKDNIDPIYITPFG-----SGPRNCIGRMFALNMKALIRVLQNFSPFK 467

RESULT 8
US-10-732-923-1079
; Sequence 1079, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149

; APPLICANT: Midgley, Carol
; TITLE OF INVENTION: Cell Cycle Progression Proteins
; FILE REFERENCE: P0158190 CYK
; CURRENT APPLICATION NUMBER: US/10/745,237
; CURRENT FILING DATE: 2003-12-23
; PRIOR APPLICATION NUMBER: US 60/439,123
; PRIOR FILING DATE: 2003-01-10
; PRIOR APPLICATION NUMBER: US 60/468,402
; PRIOR FILING DATE: 2003-05-06
; NUMBER OF SEQ ID NOS: 600
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 408
; LENGTH: 503
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: P08684
US-10-745-237-408

Query Match      13.9%; Score 396.5; DB 4; Length 503;
Best Local Similarity 28.7%; Pred. No. 2.5e-24;
Matches 153; Conservative 88; Mismatches 195; Indels 97; Gaps 24;

QY 13 LAAFSW--ASIAFFSLYLAPRRS--SLYNLQ--PNHTNY--FTGNFLDILSARTG-----E 61
Db 7 LAMETWLLAVSLVLLYLYGTHSHGLFKGLGIPGTPLPFLGN---ILSYHKGFCMFDM 63
QY 62 EHAKYREKYGSTLRFAGIAGAPVLNSTDPKVFNHVM--KEAYDY---PKPGMAARVLRIAT 117
Db 64 CHKKGKVGWGF---YDG--QQPVLAITDPMIKTVLVKECVSVFTNRRPFGVGMKSA- 117
QY 118 GGVVTAEGEAHKHRRIMIPSLSAQAVKSMVPIFLEKGMELVDKMDAEDAKDMVAGES 177
Db 118 ---ISIADEEWRKLSLSPTFTSGKLKEMVPIIAQYGDVLVRLNREA----- 164
QY 178 AGEKKATRLT--EGVDVKDWVGRATLDVMALAGFDYKSDSLQNKTNELYVAFVGLTDGFA 236
Db 165 -----ETGKPVTLKDVFGAYSMDVITSTSGVNIIDSLNNPD----- 201
QY 237 PTLDSFKAIM-WDFV-PYFRTMK--RRHEIPLTQGLAV---SRRVGIELMEQKQAVLGSA 290
Db 202 PFVENTKLLRFDLDPFPLSITVPFPLIPILEVNLICVFPREVTFNLRKSVKR-----M 256
QY 291 SDQAVDKDQVGRDILSLVRANIAANLPESQKLSDEEVLQAISNLLFAGYETSSTVLTW 350
Db 257 KESRLDQTKHRVDFQLMIDSONSKETESHKALSDELVAQSIIPIFAGYETTSVLSF 316
QY 351 MFHRLSEDKAVQDKLREEICQI--DTPMTLDLDELNALPYLEAFVKESLRDPPSPYANRE 408
Db 317 IMVELATHPDVQOKLQEEIDAVLNPKAPPTYDVTVLQMEYLDVMVNETLRFPIAMRLERV 376
QY 409 CLKDEDFIPLAEPVIGRGSVINEVRITKGTWMLPLFNINRSKFIYGEAEFRPRERWL 468
Db 377 CKKQVE-----INGMFIPKGVWVWIPSYALHRDP-KYWTPEKFLPERFS 420
QY 469 EDVTDLSNS-IEAPYGHQASFIQPRACFGWRFAVAEMKAFLVFTLRRVQFEP 520
Db 421 KKNKDNIDPIYITPFG-----SGPRNCIGRMFALNMKALIRVLQNFSPFK 467

RESULT 7
US-10-745-237-408
; Sequence 408, Application US/10745237
; Publication No. US20050227301A1
; GENERAL INFORMATION:
; APPLICANT: Cyclacel Limited
; APPLICANT: Glover, David
; APPLICANT: Bell, Graham
; APPLICANT: Frenz, Lisa

```

```
; SEQ ID NO 1079
; LENGTH: 503
; TYPE: PRT
; ORGANISM: Macaca fascicularis
US-10-732-923-1079

Query Match      13.9%; Score 395.5; DB 5; Length 503;
Best Local Similarity 28.6%; Pred. No. 3e-24;
Matches 155; Conservative 85; Mismatches 187; Indels 115; Gaps 26;

QY 13 LAAFSW--ASTAFSLYLAPRR--SLYNLQ--PNHTNY--FTGNFLDILSARTG-----E 61
Db 7 LAVETWLLAVTLVLLYLYGTHSHGLFKKLGPGTLPPLGN---ILSYRKGPWTFDME 63
QY 62 BHAKYREKYGSTLRFAGIAGAPVLNSTDPKVFNVHM--KEAYD-----YKPGMAARVL 113
Db 64 CYKYGKVGWGF---YDG--RQPVLAITDPNMIKTVLKCEYSVFTNRRPFGVFGMKNAI 118
QY 114 RIATGCVVTAEGEAHKKHRRIMIPSLSAQAVKSMVPIFEKGMELVDKXMDAAEKDMA 173
Db 119 SI-----AEDEEWKIRSLLSPTFTSGKLKEMVPIIAKYGDVLRNLREA----- 164
QY 174 VGESAGEKKATRLT-EGVDVKDWVGRATLDVMALAGFDYKSDSLQNKTNELNYVAFGLT 232
Db 165 -----ETGKPVTLKDVFGAYSMVDITSTSGVNIIDSLNPD----- 201
QY 233 DGFAPTLDSFKAIM-WDFV-PYFRMK-RRHEIPLTOGLAVS---RRVGIEMLSQKQAV 286
Db 202 ---PFVENTKLLRFDLPDPFLLSITTFPIIPILEVLTNISPPEVTSFLRSKVRKI- 256
QY 287 LGSASDAQVDKQVGR--DILSLVRANIAANLPSQKLSDEEVLAQISNLLFAGYETS 344
Db 257 -----KESRLKQTKGRVDFLQLMIDSONSKETESHKALSDELVASQSIIFIFAGYETT 310
QY 345 STVLTMFHLRSEDKAVQDKLREEICQIDTDM-----PTLDELNALPYLEAFVKSRLD 399
Db 311 SSVLSFIYELATHPDVQKQEE---IDTVLPNKAPTYDTVLQMEYLDVMVNETLRIF 367
QY 400 PPSVYANRECLKDEDFIPLAEPIVGRDGSVINEVRITKGTWMLPLFNINRSKFYIGDA 459
Db 368 PIAMLERVCKDVE-----INGFIPIKGVVVMIPSYALHHPD-KYWDEP 411
QY 460 BEFRERWLEDVTDLSNS-IEAPYGHQASFTSGPRACFGWRFVAFVAKFLVTLRRVQF 518
Db 412 EKFLPERFSKKNNDIDPIYITPFG-----SGPRNCIGMRPALNMKLAIRVLQNSF 465
QY 519 EP 520
Db 466 KP 467

RESULT 9
US-10-690-991-2
; Sequence 2, Application US/10690991
; Publication No. US2004024319A1
; GENERAL INFORMATION:
; APPLICANT: Tickle, Ian J
; APPLICANT: Vonrhein, Clemens
; APPLICANT: Williams, Pamela A
; APPLICANT: Jhoti, Harren
; APPLICANT: Kirtson, Stewart Brian
; TITLE OF INVENTION: Crystal structure of cytochrome P450
; FILE REFERENCE: 620-282
; CURRENT APPLICATION NUMBER: US/10/690,991
; CURRENT FILING DATE: 2004-04-13
; PRIOR APPLICATION NUMBER: US 60/421,063
; PRIOR FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: PCT/GB02/02668
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: US 10/221,036
; PRIOR FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: US 60/479,448
; PRIOR FILING DATE: 2003-06-19
```

```
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 2
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Human 3A4 P450 protein truncated in its N-terminal region to
; delete the hydrophobic trans-membrane domain, and the region
; OTHER INFORMATION: replaced by a short N-terminal sequence.
US-10-690-991-2

Query Match      13.8%; Score 394; DB 5; Length 485;
Best Local Similarity 28.7%; Pred. No. 3.8e-24;
Matches 142; Conservative 83; Mismatches 177; Indels 92; Gaps 20;

QY 47 FTGNFLDILSARTG-----EEHAKYREKYGSTLRFAGIAGAPVLNSTDPKVFNVHM-KE 99
Db 24 FLGN---ILSYHKGFCDMECHKKYGKVGWGF---YDG--QOPVLAITDPDMIKTVLVKE 75
QY 100 AYDY---PKPGMAARVLRIATGCVVTAEGEAHKKHRRIMIPSLSAQAVKSMVPIFEKLG 156
Db 76 CYSVFTNRRPFGVFGMKSA-----ISAEDEEWKRLSLSPFTTSKGLKEMVPIIAQYG 131
QY 157 MELVDKXMDAAEKDMAVGESAGEKKATRLT-EGVDVKDWVGRATLDVMALAGFDYKSD 215
Db 132 DVLVRNLREA-----ETGKPVTLKDVFGAYSMVDITSTSGVNIID 172
QY 216 SLQNKTNELNYVAFGLTDFGAPTLDSFKAIM-WDFV-PYFRMK-RRHEIPLTOGLAV-- 270
Db 173 SLNPDQ-----PFVENTKLLRFDLPDPFLLSITTFPIIPILEVLTNID 218
QY 271 -SRVGIEMLSQKQAVLGSASDAQVDKQVGRDILSLVRANIAANLPSQKLSDEEVL 329
Db 219 FPREVTNPLRSKVR-----MKESRLKQTKGRVDFLQLMIDSONSKETESHKALSDELV 273
QY 330 LAQISNLLFAGYETSSTVLTMFHLRSEDKAVQDKLREEICQI---DTDMPTLDELNALPY 387
Db 274 VAQSIIFIFAGYETTSVLSFIYELATHPDVQKQEEIDAVLPNKAPTYDTVLQMEY 333
QY 388 LEAFVKSRLDPPSPYANRECLKDEDFIPLAEPIVGRDGSVINEVRITKGTWMLPLFN 447
Db 334 LDMVNETLRFLPIAMLERVCKDVE-----INGFIPIKGVVVMIPSYA 378
QY 448 INRSKFYIGDAEERFERWLEDVTDLSNS-IEAPYGHQASFTSGPRACFGWRFVAFVAKM 506
Db 379 LHRDP-KYWTPEKFLPERFSKKNNDIDPIYITPFG-----SGPRNCIGMRPALNMK 431
QY 507 AFLFVTLRRVQFEP 520
Db 432 LALIRVLQNSF 445

RESULT 10
US-10-833-296-2
; Sequence 2, Application US/10833296
; Publication No. US20050032119A1
; GENERAL INFORMATION:
; APPLICANT: Tickle, Ian J
; APPLICANT: Vonrhein, Clemens
; APPLICANT: Vinkovic, Dijana M
; APPLICANT: Kirtson, Stewart
; APPLICANT: Williams, Pamela A
; APPLICANT: Jhoti, Harren
; TITLE OF INVENTION: Crystal Structure of Cytochrome P450
; FILE REFERENCE: 620-305
; CURRENT APPLICATION NUMBER: US/10/833,296
; CURRENT FILING DATE: 2004-04-28
; PRIOR APPLICATION NUMBER: GB 0108214.8
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: GB 0108212.2
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: US 60/479,448
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; PRIOR FILING DATE: 2003-06-19  
; PRIOR APPLICATION NUMBER: US 60/421,063  
; PRIOR FILING DATE: 2002-10-25  
; PRIOR APPLICATION NUMBER: US 60/306,873  
; PRIOR FILING DATE: 2001-07-23  
; PRIOR APPLICATION NUMBER: US 60/306,874  
; PRIOR FILING DATE: 2001-07-23  
; PRIOR APPLICATION NUMBER: US 10/690,991  
; PRIOR FILING DATE: 2003-10-23  
; PRIOR APPLICATION NUMBER: US 10/221,036  
; PRIOR FILING DATE: 2002-04-02  
; PRIOR APPLICATION NUMBER: PCT/GB02/02668  
; PRIOR FILING DATE: 2002-05-30  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 485  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Human 3A4 P450 protein truncated in its N-terminal region  
; OTHER INFORMATION: to delete the hydrophobic trans-membrane domain, and the  
; OTHER INFORMATION: region replaced by a short N-terminal sequence.  
US-10-833-296-2

Query Match 13.8%; Score 394; DB 5; Length 485;  
Best Local Similarity 28.7%; Pred. No. 3.8e-24;  
Matches 142; Conservative 83; Mismatches 177; Indels 92; Gaps 20;  
QY 47 FTGNFLDILSARTG-----BEHAKYREKYSTLRFAAGIAGAPVLNSTDPKVFNVHM-KE 99  
Db 24 FLGN---ILSYHKGFDMCHKYGKVGWGF---YDG--QQPVLAITDPDMIKTVLVE 75  
QY 100 AYDY---PKPGMAARVLRATGDGVTVAEGEAHRRHIMIPSLSAQAQVKSMPVIFLEKG 156  
Db 76 CYSVFTNRPPGPGVGMKSA-----ISIAEDBEWKRLSLSPFTTSGLKEMVPIIAQYG 131  
QY 157 MELVDKMDAAEKDMAGVSGESAGEKKATRLT-EGVDVKDWVGRATLDVMAAGFDYKSD 215  
Db 132 DVLVRLNRREA-----ETGKPVTLKDVFGAYSMDVITSTSGVNVNID 172  
QY 216 SLQNKTNELVYAFVGLTGDGFAPTLDSFKAIM-WDFV-PYFRMK-RRHEIPLTQGLAV-- 270  
Db 173 SLNNPQD-----PFVENTKLLRFDLDFLSPFTTSGLKEMVPIIAQYG 218  
QY 271 -SRRVGIEMEQKQAVLGSASDAQVDKQVGRDILSLVRANIAANLPSQKLSDEEV 329  
Db 219 FPREVTFNLRKSVKR-----MKSRLDTQKHRVDFLQLMIDSONSKETESHKALSDEL 273  
QY 330 LAQISNLLPAGYETSTVLTWTFHRLSEDKAVQDKLREEICQI--DTDMPTLDLNLALPY 387  
Db 274 VAQSIIFIFAGYETTSVLSFIMYELATHPDVQVKLQEEIDAVLPNKAPPTDVLQMEY 333  
QY 388 LEAFVKESLRDPPSPYANRECLKDEDFIPLAEPVIGRDSVINEVRITKGTVMVLPFN 447  
Db 334 LDMVNETLRLFPPIAMRLERVKCKDVE-----INGMFIKPGVVMVIPSYA 378  
QY 448 INRSKFIYGEDAEFRPERWLEDVTDLSNS-IEAPYGHQASFIISGPRACFGWRFAVEMK 506  
Db 379 LHRDP-KYWTPEKFLPERFSKKNKNDIPYITPFG-----SGPRNCIGMRFALNMWK 431  
QY 507 AFLFVTLRRVQFEP 520  
Db 432 LALIRVLQNFSPK 445

## RESULT 11

US-10-516-338-8  
; Sequence 8, Application US/10516338  
; Publication No. US20050164341A1  
; GENERAL INFORMATION:  
; APPLICANT: Astex Technology Limited  
; APPLICANT: Cosme, Jose

; APPLICANT: Ward, Alison  
; APPLICANT: Vuillard, Laurent  
; APPLICANT: Williams, Pamela  
; APPLICANT: Hamilton, Bruce  
; TITLE OF INVENTION: Methods of Purification of Cytochrome P450 Proteins  
; FILE REFERENCE: AHBCP6047252  
; CURRENT APPLICATION NUMBER: US/10/516,338  
; CURRENT FILING DATE: 2004-11-30  
; NUMBER OF SEQ ID NOS: 84  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 8  
; LENGTH: 485  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: 3A4  
US-10-516-338-8

Query Match 13.8%; Score 394; DB 5; Length 485;  
Best Local Similarity 28.7%; Pred. No. 3.8e-24;  
Matches 142; Conservative 83; Mismatches 177; Indels 92; Gaps 20;  
QY 47 FTGNFLDILSARTG-----ESHAKYREKYSTLRFAAGIAGAPVLNSTDPKVFNVHM-KE 99  
Db 24 FLGN---ILSYHKGFDMCHKYGKVGWGF---YDG--QQPVLAITDPDMIKTVLVE 75  
QY 100 AYDY---PKPGMAARVLRATGDGVTVAEGEAHRRHIMIPSLSAQAQVKSMPVIFLEKG 156  
Db 76 CYSVFTNRPPGPGVGMKSA-----ISIAEDBEWKRLSLSPFTTSGLKEMVPIIAQYG 131  
QY 157 MELVDKMDAAEKDMAGVSGESAGEKKATRLT-EGVDVKDWVGRATLDVMAAGFDYKSD 215  
Db 132 DVLVRLNRREA-----ETGKPVTLKDVFGAYSMDVITSTSGVNVNID 172  
QY 216 SLQNKTNELVYAFVGLTGDGFAPTLDSFKAIM-WDFV-PYFRMK-RRHEIPLTQGLAV-- 270  
Db 173 SLNNPQD-----PFVENTKLLRFDLDFLSPFTTSGLKEMVPIIAQYG 218  
QY 271 -SRRVGIEMEQKQAVLGSASDAQVDKQVGRDILSLVRANIAANLPSQKLSDEEV 329  
Db 219 FPREVTFNLRKSVKR-----MKSRLDTQKHRVDFLQLMIDSONSKETESHKALSDEL 273  
QY 330 LAQISNLLPAGYETSTVLTWTFHRLSEDKAVQDKLREEICQI--DTDMPTLDLNLALPY 387  
Db 274 VAQSIIFIFAGYETTSVLSFIMYELATHPDVQVKLQEEIDAVLPNKAPPTDVLQMEY 333  
QY 388 LEAFVKESLRDPPSPYANRECLKDEDFIPLAEPVIGRDSVINEVRITKGTVMVLPFN 447  
Db 334 LDMVNETLRLFPPIAMRLERVKCKDVE-----INGMFIKPGVVMVIPSYA 378  
QY 448 INRSKFIYGEDAEFRPERWLEDVTDLSNS-IEAPYGHQASFIISGPRACFGWRFAVEMK 506  
Db 379 LHRDP-KYWTPEKFLPERFSKKNKNDIPYITPFG-----SGPRNCIGMRFALNMWK 431  
QY 507 AFLFVTLRRVQFEP 520  
Db 432 LALIRVLQNFSPK 445

## RESULT 12

US-11-076-967-2  
; Sequence 2, Application US/11076967  
; Publication No. US20050159901A1  
; GENERAL INFORMATION:  
; APPLICANT: tickle, Ian J  
; APPLICANT: Vornheim, Clemens  
; APPLICANT: Williams, Pamela A  
; APPLICANT: Jhoti, Harren  
; APPLICANT: Kirtan, Stewart Brian  
; TITLE OF INVENTION: Crystal structure of cytochrome P450  
; FILE REFERENCE: 620-282  
; CURRENT APPLICATION NUMBER: US/11/076,967  
; CURRENT FILING DATE: 2005-03-11

;; PRIOR APPLICATION NUMBER: US/10/690,991  
;; PRIOR FILING DATE: 2003-10-23  
;; PRIOR APPLICATION NUMBER: US 60/421,063  
;; PRIOR FILING DATE: 2002-10-25  
;; PRIOR APPLICATION NUMBER: PCT/GB02/02668  
;; PRIOR FILING DATE: 2002-05-30  
;; PRIOR APPLICATION NUMBER: US 10/221,036  
;; PRIOR FILING DATE: 2002-04-02  
;; PRIOR APPLICATION NUMBER: US 60/479,448  
;; PRIOR FILING DATE: 2003-06-19  
;; NUMBER OF SEQ ID NOS: 6  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 2  
;; LENGTH: 485  
;; TYPE: PRT  
;; ORGANISM: Artificial sequence  
;; FEATURE:  
;; OTHER INFORMATION: Human 344 P450 protein truncated in its N-terminal region to  
;; OTHER INFORMATION: delete the hydrophobic trans-membrane domain, and the region  
;; OTHER INFORMATION: replaced by a short N-terminal sequence.  
US-11-076-967-2

Query Match 13.8%; Score 394; DB 6; Length 485;  
Best Local Similarity 28.7%; Pred. No. 3.8e-24;  
Matches 142; Conservative 83; Mismatches 177; Indels 92; Gaps 20;  
Qy 47 FTGNFLDILSARTG-----EEHAKYREKYGSTLRFGIAGAPVLNSTDPKVFNNHM-KE 99  
Db 24 FLGN---ILSYHKGFCDMECHKYKGVGF---YDG--QQPVLAITDPMIKTLVKE 75  
Qy 100 AYDY---PKPGMAARVLRIATGDGVVTAEGEAHRRIMIPSLSAQAVKSMVPIFEKG 156  
Db 76 CYSVFTNRPRPGVGFMKSA-----ISIAEDEEWKRLRLSLLSPTFTSGKLEKEMVPIIAQYG 131  
Qy 157 MELVDKWMEDAEKDMAGVAGESAGEKATRLT-EGVDVKDWVGRATLDVMAAGFDYKSD 215  
Db 132 DVLVRLNREA-----ETGKPVTLKDVFGAYSMDVITSTFGVNID 172  
Qy 216 SLQNKNTNELYVAVGLTDGFAPTLDSFKAIM-WDFV-PYFRTMK-RRHEIPLTQGLAV-- 270  
Db 173 SLNPNQD-----PFVENTKLLRFDFLDPFFLSITVFPPLIPILEVLNFCV 218  
Qy 271 -SRRVGIELMOKQKQAVLGSASDQAVDKDVQGRDILSLVRANIAPNPSQKLSDEEV 329  
Db 219 FPREVTFNLRKSVKR-----MKESLEDTQKRVDFLQMLIDSQNSKETESHKALSDEL 273  
Qy 330 LAQISNLLFAGVETSSVLTWTFHRLSEDKAVQDKLREEICQI--DTDMPTLDLDELNALPY 387  
Db 274 VAQSIIFIFAGVETSSVLSFIMYELATHPDVQQLQEEIDAVLPNKAPPTVDVLQMEY 333  
Qy 388 LEAFVKESLRDPPSPYANRECKDDEDFIPLAEPVIGRDGVSINEVRITKGTVMVPLFN 447  
Db 334 LDMVNETLRUFFIAMRLERVCKDVE-----INGMFIPKGVVVMIPSYA 378  
Qy 448 INRSKFIYGEDAEERPRERWLEDVTDLSNLS-IEAPYGHQASFISGPRACFGWRFAVAMK 506  
Db 379 LHRDP-KYWTPEKEFLPERFSKKNKNDIPYITPFG-----SGPRNCIGRFAALMMNK 431  
Qy 507 AFLFTVLRVQPEP 520  
Db 432 LALIRVLQNFSPK 445

RESULT 13  
US-10-425-115-294241  
; Sequence 294241, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

;; TITLE OF INVENTION: Plants  
;; FILE REFERENCE: 38-21(53222)B  
;; CURRENT APPLICATION NUMBER: US/10/425,115  
;; CURRENT FILING DATE: 2003-04-28  
;; NUMBER OF SEQ ID NOS: 369326  
;; SEQ ID NO 294241  
;; LENGTH: 543  
;; TYPE: PRT  
;; ORGANISM: Zea mays  
;; FEATURE:  
;; NAME/KEY: unsure  
;; LOCATION: (1)..(543)  
;; OTHER INFORMATION: unsure at all xaa locations  
;; FEATURE:  
;; OTHER INFORMATION: Clone ID: MRT4577\_31433C.1.pep  
US-10-425-115-294241

Query Match 13.8%; Score 392.5; DB 4; Length 543;  
Best Local Similarity 26.1%; Pred. No. 6e-24;  
Matches 150; Conservative 95; Mismatches 226; Indels 103; Gaps 23;  
Qy 6 LLTGALGLAAPSWSAIAPFSL-----YLAPRRSLYNLOGPNHTNYPTGNFELDILSARTG- 60  
Db 22 MVAATAVAALASWAFNALVHLVMPYAITRLRAQGVGRPPYT--FFTGSIGLEIKRLRAEG 80  
Qy 61 -----EEH-----AKYREKYGSTLRFGIAGA-PVLNSTDPKVFNNHMKAYD 102  
Db 81 AAVTLVDVDDHDFPMVQPHLRKWIALLYGRT--FYWTGARPNVCVADVNVVRVL---FD 135  
Qy 103 ----YKPGMAARVLRIATGDGVVTAEGEAHRRIMIPSLSAQAVKSMVPIFEKGM 158  
Db 136 RTGLYKPNLNPILPHISRL-LCKGLVLTGDDDKRHKRVVHPAFNMDKLMATMTSDCTRS 194  
Qy 159 LVDKQMEDAAEKDMAGVAGESAGEKATRLTEGVVDKDWVGRATLDVMAAGFDYKSDSLQ 218  
Db 195 MISEWDAQLOKED-----QSGRGHGHVHE---VELSSRFBELTADVISHTAF----GSSY 242  
Qy 219 NKTNELYVAVGLTDGFAPTLDSFKAIMWDFVFPYFRTMKRRHEIPLTQGLAVSRVRIEL 278  
Db 243 NEGKRVFLARELOH-----IAFSTIP-----NVQIPALKYLPTEKNLRTRK 284  
Qy 279 MEQKKQAVLGSASDQAVDKKDV---QGRDILSLVRANIAPNPSQ-----KLSDEEV 329  
Db 285 LDRQVRAMLMDIIEARLASKDTAGGYGNLLGLMLEA--CASPEHHEGEMAPTTLSDMEI 342  
Qy 330 LAQISNLLFAGVETSSVLTWTFHRLSEDKAVQDKLREEI---CQIDTDMPTLDLDELNALP 386  
Db 343 VDECKTFFAGHDTTSHLTWASFLSTHPWQHRLRDEVRRREGC-DDEVPTGDALNRLK 401  
Qy 387 YLEAFVKESLRDPPSPYANRECKDDEDFIPLAEPVIGRDGVSINEVRITKGTVMVPLF 446  
Db 402 LVNMFLETLLKLYGPVSLIQRKAGSDLD-----LGGIRVPSGAILTIRLA 446  
Qy 447 NINRSKFIYGEDAEERPRERWLEDVTDLSNLSIEAPYGHQASFISGPRACFGWRFAVAMK 506  
Db 447 TIXRDKVWGEDAGEFRLEFRFENGVTAAAKHPNA----LLSFSGSPRSCIGNFAMIEAK 502  
Qy 507 AFLFTVLRVQPEPIIISHPEYEH--ITLIISRPR 538  
Db 503 AVAMILQRFALE---LSPKYVHAPMDLITLRPR 533

RESULT 14  
US-10-751-235-35  
; Sequence 35, Application US/10751235  
; Publication No. US20050150002A1  
; GENERAL INFORMATION:  
; APPLICANT: Dellapenna, Dean  
; APPLICANT: Tian, Li  
; APPLICANT: Kim, Joonyul  
; TITLE OF INVENTION: Novel Carotenoid Hydroxylases for Use in Engineering Carotenoid  
; TITLE OF INVENTION: Metabolism in Plants  
; FILE REFERENCE: MSU-08604



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 21, 2005, 16:52:36 ; Search time 26 seconds  
(without alignments)  
1771.167 Million cell updates/sec

Title: US-10-066-007A-1

Perfect score: 2852

Sequence: 1 MFILVLTGALGLAASFWSAS.....RIVGREKEGYQMLQVXPVE 557

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.\*

- 1: /cgn2\_6/ptodata/1/iaa/5 COMB.pdp.\*
- 2: /cgn2\_6/ptodata/1/iaa/6 COMB.pdp.\*
- 3: /cgn2\_6/ptodata/1/iaa/H COMB.pdp.\*
- 4: /cgn2\_6/ptodata/1/iaa/PCTUS COMB.pdp.\*
- 5: /cgn2\_6/ptodata/1/iaa/RE COMB.pdp.\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles.pdp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2852	100.0	557	2	US-09-518-386B-1
2	2852	100.0	557	2	US-09-518-386B-3
3	398.5	14.0	508	2	US-09-949-016-7092
4	398.5	14.0	508	2	US-09-949-016-8562
5	396.5	13.9	503	2	US-09-144-367-2
6	385.5	13.5	508	2	US-09-949-016-8561
7	385	13.5	502	2	US-09-949-016-5992
8	385	13.5	507	2	US-09-949-016-7091
9	370	13.0	504	1	US-08-457-274A-25
10	370	13.0	504	4	PCT-US95-05758-25
11	367	12.9	520	2	US-09-527-073-2
12	350	12.3	527	2	US-09-949-016-10078
13	346.5	12.1	524	2	US-09-991-181-264
14	346.5	12.1	524	2	US-09-990-444-264
15	346.5	12.1	524	2	US-09-997-333-264
16	346.5	12.1	524	2	US-09-992-598-264
17	345	12.1	524	2	US-09-976-594-533
18	344	12.1	520	2	US-09-949-016-6003
19	338.5	11.9	503	2	US-09-583-447A-2
20	331	11.6	540	2	US-09-302-620B-99
21	330.5	11.6	507	1	US-08-457-274A-22
22	330.5	11.6	507	4	PCT-US95-05758-22
23	328	11.5	504	2	US-09-583-447A-4
24	328	11.5	540	2	US-09-302-620B-98
25	326.5	11.4	541	2	US-09-158-767-19
26	326.5	11.4	541	2	US-09-158-767-20
27	326.5	11.4	541	2	US-09-713-794-19

28	326.5	11.4	541	2	US-09-713-794-20	Sequence 20, Appl
29	321	11.3	576	2	US-08-948-564-16	Sequence 16, Appl
30	320.5	11.2	529	2	US-09-270-767-46468	Sequence 46468, A
31	318.5	11.2	526	1	US-08-298-426-4	Sequence 4, Appl
32	315	11.0	1049	2	US-10-018-730A-4	Sequence 4, Appl
33	304.5	10.7	436	2	US-09-902-540-12913	Sequence 12913, A
34	301.5	10.6	475	2	US-09-710-262E-13	Sequence 13, Appl
35	294.5	10.3	489	2	US-09-852-067-4	Sequence 4, Appl
36	294.5	10.3	489	2	US-10-338-691-4	Sequence 4, Appl
37	294	10.3	522	2	US-09-302-620B-97	Sequence 97, Appl
38	289	10.1	522	2	US-09-302-620B-96	Sequence 96, Appl
39	287.5	10.1	536	2	US-09-949-016-10134	Sequence 10134, A
40	286	10.0	548	2	US-09-248-796A-15537	Sequence 15537, A
41	278.5	9.8	507	2	US-09-248-796A-15540	Sequence 15540, A
42	276	9.7	420	2	US-09-583-447A-6	Sequence 6, Appl
43	276	9.7	467	2	US-09-126-420A-17	Sequence 17, Appl
44	273.5	9.6	500	2	US-09-949-016-7973	Sequence 7973, Ap
45	273.5	9.6	513	2	US-09-949-016-5993	Sequence 5993, Ap

## ALIGNMENTS

### RESULT 1

US-09-518-386B-1

; Sequence 1, Application US/09518386B

; Patent No. 6365386

; GENERAL INFORMATION:

; APPLICANT: HOSHINO, Tatsuo

; APPLICANT: OJIMA, Kazuyuki

; APPLICANT: SETOGUCHI, Yutaka

; TITLE OF INVENTION: ASTAXANTHIN SYNTHETASE

; FILE REFERENCE: ASTAXANTHIN SYNTHETASE

; CURRENT APPLICATION NUMBER: US/09/518.386B

; CURRENT FILING DATE: 2000-03-03

; PRIOR APPLICATION NUMBER: EP 99104668.1

; PRIOR FILING DATE: 1999-03-09

; PRIOR APPLICATION NUMBER: EP 00101666.6

; PRIOR FILING DATE: 2000-02-01

; NUMBER OF SEQ ID NOS: 32

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1

; LENGTH: 557

; TYPE: PRT

; ORGANISM: Phaffia rhodozyma

; FEATURE:

; NAME/KEY: TRANSIT

; LOCATION: (1)..(26)

US-09-518-386B-1

Query Match 100.0%; Score 2852; DB 2; Length 557;

Best Local Similarity 100.0%; Pred. No. 3.2e-277;

Matches 557; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MFILVLTGALGLAASFWSASIAFFSLYAPRRSSLYNLOGPNHNTNYFTGNFIDLISARTG	60
Db	1	MFILVLTGALGLAASFWSASIAFFSLYAPRRSSLYNLOGPNHNTNYFTGNFIDLISARTG	60
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Db	61	BEHAKYREKYGSTLRFAGIAGAPVLNSTDPKVFNVHVKAEYDYPKPGMAARVLRATG	120
Qy	121	VVTAEGEAKHRRRIMIPSLSAQAVKSNVPFLEKGMELVDKMMEDAAEKDMVAGESAGE	180
Db	121	VVTAEGEAKHRRRIMIPSLSAQAVKSNVPFLEKGMELVDKMMEDAAEKDMVAGESAGE	180
Qy	181	KKATRLTEGVVDKDWVGRATLDVMAAGFDYKSDSLQNKTNELVAVFVGLTDGFAPLTD	240
Db	181	KKATRLTEGVVDKDWVGRATLDVMAAGFDYKSDSLQNKTNELVAVFVGLTDGFAPLTD	240
Qy	241	SFKAIMDVFVYFRTMKRHEIPTQGLAVSRVRVGIEMEQKQAVLGSASDAQVKKDV	300
Db	241	SFKAIMDVFVYFRTMKRHEIPTQGLAVSRVRVGIEMEQKQAVLGSASDAQVKKDV	300

*part came*



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Qy 301 QGRDILSLVRANIAANLPESQKLSDEVLQAISNLLFAGYETSSVTLTWTFHRLSBDKA 360
Db 301 QGRDILSLVRANIAANLPESQKLSDEVLQAISNLLFAGYETSSVTLTWTFHRLSBDKA 360
Qy 361 VQDKLREEICQIDTDMPTLDELNALPYLEAFVKESLRLDPPSPYANRECLKDDEFIPLAE 420
Db 361 VQDKLREEICQIDTDMPTLDELNALPYLEAFVKESLRLDPPSPYANRECLKDDEFIPLAE 420
Qy 421 PVIGRDSGVINEVRITKGTWVWMLPLFNINRSKFIYGEDAEERPERWLEDTVDSLSNIEA 480
Db 421 PVIGRDSGVINEVRITKGTWVWMLPLFNINRSKFIYGEDAEERPERWLEDTVDSLSNIEA 480
Qy 481 PYGHOASFTSGPRACFGWRFAVAKMAFLFVTLRRVQFEPILISHPEYEHITLIISRPRIV 540
Db 481 PYGHOASFTSGPRACFGWRFAVAKMAFLFVTLRRVQFEPILISHPEYEHITLIISRPRIV 540
Qy 541 GREKEGYQMRLOQKPV 557
Db 541 GREKEGYQMRLOQKPV 557

RESULT 2
US-09-518-386B-3
; Sequence 3, Application US/09518386B
; Patent No. 6365386
; GENERAL INFORMATION:
; APPLICANT: HOSHINO, Tatsuo
; APPLICANT: OJIMA, Kazuyuki
; APPLICANT: SETOGUCHI, Yutaka
; TITLE OF INVENTION: ASTAXANTHIN SYNTHETASE
; FILE REFERENCE: ASTAXANTHIN SYNTHETASE
; CURRENT APPLICATION NUMBER: US/09/518,386B
; CURRENT FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: EP 99104668.1
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: EP 00101666.6
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 557
; TYPE: PRT
; ORGANISM: Phaffia rhodozyma
US-09-518-386B-3

Query Match 100.0%; Score 2852; DB 2; Length 557;
Best Local Similarity 100.0%; Pred. No. 3.2e-277;
Matches 557; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFILVLLTGALGLAASFWSIAFFSLYLAPRRSSLYNLQGNHTNYTGTGNFLDLSARTG 60
Db 1 MFILVLLTGALGLAASFWSIAFFSLYLAPRRSSLYNLQGNHTNYTGTGNFLDLSARTG 60
Qy 61 EEHAKYREKYGSTLRFAGIAGAPVLNSTDPKVFNVHMKAEYDYPKPGMAARVLRIATGDG 120
Db 61 EEHAKYREKYGSTLRFAGIAGAPVLNSTDPKVFNVHMKAEYDYPKPGMAARVLRIATGDG 120
Qy 121 VVTAEGEAHKRRHRIIMIPSLSAQAVKSMVPIFLEKGMELVDKMMEDAAEKDMAVGESAGE 180
Db 121 VVTAEGEAHKRRHRIIMIPSLSAQAVKSMVPIFLEKGMELVDKMMEDAAEKDMAVGESAGE 180
Qy 181 KKATRLTEGVVDVWDVGRATLDVWALAGFDYKSDSLQNKTNELVYAFVGLTGTGFAPTLT 240
Db 181 KKATRLTEGVVDVWDVGRATLDVWALAGFDYKSDSLQNKTNELVYAFVGLTGTGFAPTLT 240
Qy 241 SFKAIMWDFVPYFTMKRRHEIPIQTQGLAVSRRVGIEMEOKKQAVLGSASDQAVDKDV 300
Db 241 SFKAIMWDFVPYFTMKRRHEIPIQTQGLAVSRRVGIEMEOKKQAVLGSASDQAVDKDV 300
Qy 301 QGRDILSLVRANIAANLPESQKLSDEVLQAISNLLFAGYETSSVTLTWTFHRLSBDKA 360
Db 301 QGRDILSLVRANIAANLPESQKLSDEVLQAISNLLFAGYETSSVTLTWTFHRLSBDKA 360
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Qy 361 VQDKLREEICQIDTDMPTLDELNALPYLEAFVKESLRLDPPSPYANRECLKDDEFIPLAE 420
Db 361 VQDKLREEICQIDTDMPTLDELNALPYLEAFVKESLRLDPPSPYANRECLKDDEFIPLAE 420
Qy 421 PVIGRDSGVINEVRITKGTWVWMLPLFNINRSKFIYGEDAEERPERWLEDTVDSLSNIEA 480
Db 421 PVIGRDSGVINEVRITKGTWVWMLPLFNINRSKFIYGEDAEERPERWLEDTVDSLSNIEA 480
Qy 481 PYGHOASFTSGPRACFGWRFAVAKMAFLFVTLRRVQFEPILISHPEYEHITLIISRPRIV 540
Db 481 PYGHOASFTSGPRACFGWRFAVAKMAFLFVTLRRVQFEPILISHPEYEHITLIISRPRIV 540
Qy 541 GREKEGYQMRLOQKPV 557
Db 541 GREKEGYQMRLOQKPV 557

RESULT 3
US-09-949-016-7092
; Sequence 7092, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C0001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7092
; LENGTH: 508
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7092

Query Match 14.0%; Score 398.5; DB 2; Length 508;
Best Local Similarity 28.1%; Pred. No. 6.9e-31;
Matches 152; Conservative 92; Mismatches 202; Indels 95; Gaps 23;

Qy 3 ILVLLTGALGLAASFWSIAFFSLYLAPRRS-SLYNLQGNHTNY-PTGNFLDLSART 59
Db 4 VVWALIPDLAMETWLLAVSLVLLYLYGTHSHGLPKKLGIPGPTLPFLGN---ILSYHK 60
Qy 60 G-----EBHAKYREKYGSTLRFAGIAGAPVLNSTDPKVFNVHMKAEYDYPKPGMA 109
Db 61 GFCWFMCECHKYKGVWGF---YDG--QQPVLAITDPDMIKTVLVKECYSVFTNRPPGP 115
Qy 110 ARVLRIATGDGVVVTASGEAHHKRRHRIIMIPSLSAQAVKSMVPIFLEKGMELVDKMMEDAAE 169
Db 116 VGPMSKA-----ISIADDEWKRSLRSLSTPTTSGLKKEWPIIAQGDVULVRNLRREA-- 169
Qy 170 KDMAVGESAGEKKATRLLET-EGVDVWDVGRATLDVWALAGFDYKSDSLQNKTNELVYAF 228
Db 170 -----ETGKPVTLKDVFGAYSDMVIITSTSGVWIDSLNNPD----- 206
Qy 229 VGLTGTGFAPTLTDSFKAIM-WDFV-PYFRIMK-RRHEIPIQTQGLAV---SRRVGIEMEOK 282
Db 207 -----PFVENTKKLLRFDFLDPFLSITTFPFLPILEVLNLCVFFPREVTNFRKSV 258
Qy 283 KQAVLGSASDQAVDKDVQGRDILSLVRANIAANLPESQKLSDEVLQAISNLLFAGYE 342
Db 259 KR-----MKESRLDTQKRVDFLQWIDMSQNSKETESHKALSDELVAQSIIFIFAGYE 313
Qy 343 TSSTVLTWTFHRLSBDKAVQDKLREICQI--DTDMPTLDELNALPYLEAFVKESLRLD 400
Db 343 TSSTVLTWTFHRLSBDKAVQDKLREICQI--DTDMPTLDELNALPYLEAFVKESLRLD 400
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Db 314 TTSSVLSFIMYELATHDPVQKLOEIDAVLPNKAPPTDYTLQMEYLDVMVNETLRLFP 373
Qy 401 PSPANRECLKDEDFIPLAEPVIGRDSGVINEVRITKGTWYMLPLFNINRSKFIYGEDAE 460
Db 374 IANLSEKCKKQVE-----INGMEIPKGVVVMIPSYALHRDP-KYWTEPE 417
Qy 461 EFRPERWLEDVTDLSNS-IEAPYGHQASFISSGRACFGRFAVAEMKAFIPLVTLRRVQFE 519
Db 418 KFLPERFSKKNIDPIYITPFG-----SGPRNCIGMRPALMMKALIRVLQNFSPFK 471
Qy 520 P 520
Db 472 P 472

RESULT 4
US-09-949-016-8562
; Sequence 8562, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL0011307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8562
; LENGTH: 508
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8562

Query Match
Best Local Similarity 14.0%; Score 398.5; DB 2; Length 508;
Matches 152; Conservative 92; Mismatches 202; Indels 95; Gaps 23;

Qy 3 ILVLTGALGLAFAWSIAFSLYLAPRRS-SLYNLOG-PNHTNY-FTGNFLDILSART 59
Db 4 VVMALIPDLAMETWLLAVSLVLLYLGTHSHGLFKLGIPTPLPLGN---ILSYHK 60
Qy 60 G-----EHAHYREKYGSTLRFAGIAGAPVLNSTDPKVFNVHM-KEAYDY---PKPGWA 109
Db 61 GFCFMDECHKYKGVWGF---YDG--QQPVLAITDPMIKTVLVKECVSVFTNRRPFGP 115
Qy 110 ARVLRIATGDVVTAEGEAKHRRIMIPSLSAQAVKSMVPFILEKGMELVDKMDADAE 169
Db 116 VCFMKA-----ISIADEDEWKRLSLLSPTFTSGKLKEMVPIIAQYGDVLRNLRREA-- 169
Qy 170 KDMAVGESAGEKATRLT-EGVDVKDWGRATLDVMALAGDYKSDLSQNKTNELVAF 228
Db 170 -----ETGKPVTLKDFGAYSDVITSTSGVNIIDSLNNPD----- 206
Qy 229 VGLTGTGAPTLDSFKAIM-WDFV-PYFRMTK-RRHEIPTQGLAV---SRRVGIELMEQK 282
Db 207 -----PFVENTKLLRDFLDPPFLSITVPFPIPILEVLNICVFPREVNTFLRKS 258
Qy 283 KOAVLGASDAQVDKQVGRDILSLVRANIAANLPESOKLSDEVLQAIENLLPAGYE 342
Db 259 KR-----MKESLEDQKRVDFLQMLDSQNSKETESHKALSDLELVAQSIIIFAGYE 313
Qy 343 TSSTVLTWMPHRLSEDAKQVQDLREICQI--DTMPTLDELNALPYLEAFVKESLRDLP 400
Db 314 TTSSVLSFIMYELATHDPVQKLOEIDAVLPNKAPPTDYTLQMEYLDVMVNETLRLFP 373
Qy 401 PSPANRECLKDEDFIPLAEPVIGRDSGVINEVRITKGTWYMLPLFNINRSKFIYGEDAE 460
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Db 374 IANLSEKCKKQVE-----INGMEIPKGVVVMIPSYALHRDP-KYWTEPE 417
Qy 461 EFRPERWLEDVTDLSNS-IEAPYGHQASFISSGRACFGRFAVAEMKAFIPLVTLRRVQFE 519
Db 418 KFLPERFSKKNIDPIYITPFG-----SGPRNCIGMRPALMMKALIRVLQNFSPFK 471
Qy 520 P 520
Db 472 P 472

RESULT 5
US-09-144-367-2
; Sequence 2, Application US/09144367
; Patent No. 6432639
; GENERAL INFORMATION:
; APPLICANT: Lichter, Jay
; APPLICANT: Guido, Marco
; TITLE OF INVENTION: GENOTYPING OF HUMAN CYP3A4
; FILE REFERENCE: SEQ-12P
; CURRENT APPLICATION NUMBER: US/09/144,367
; CURRENT FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 60/058,612
; PRIOR FILING DATE: 1997-09-10
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 503
; TYPE: PRT
; ORGANISM: H. sapiens
US-09-144-367-2

Query Match
Best Local Similarity 13.9%; Score 396.5; DB 2; Length 503;
Matches 153; Conservative 88; Mismatches 195; Indels 97; Gaps 24;

Qy 13 LAAPFSW--ASIAFSLYLAPRRS-SLYNLOG-PNHTNY-FTGNFLDILSARTG-----E 61
Db 7 LAMETWLLAVSLVLLYLGTHSHGLFKLGIPTPLPLGN---ILSYHKGFCMFME 63
Qy 62 EHAHYREKYGSTLRFAGIAGAPVLNSTDPKVFNVHM-KEAYDY---PKPGWAARVLRIAT 117
Db 64 CHKYYKGVWGF---YDG--QQPVLAITDPMIKTVLVKECVSVFTNRRPFGVGFMSA- 117
Qy 118 GDVVTAEGEAKHRRIMIPSLSAQAVKSMVPFILEKGMELVDKMDADAEKDMAVGES 177
Db 118 ---ISIADEDEWKRLSLLSPTFTSGKLKEMVPIIAQYGDVLRNLRREA----- 164
Qy 178 AGEKATRLT-EGVDVKDWGRATLDVMALAGDYKSDLSQNKTNELVAFVGLTGDFA 236
Db 165 -----ETGKPVTLKDFGAYSDVITSTSGVNIIDSLNNPD----- 201
Qy 237 PTLDSFKAIM-WDFV-PYFRMTK-RRHEIPTQGLAV---SRRVGIELMEQKQAVLGA 290
Db 202 PFVENTKLLRDFLDPPFLSITVPFPIPILEVLNICVFPREVNTFLRKSVKR-----M 256
Qy 291 SDQAVDKQVGRDILSLVRANIAANLPESOKLSDEVLQAIENLLPAGYETSSTVLTW 350
Db 257 KESLEDQKRVDFLQMLDSQNSKETESHKALSDLELVAQSIIIFAGYETTSVLSUF 316
Qy 351 MFHRLSEDAKQVQDLREICQI--DTMPTLDELNALPYLEAFVKESLRDLPSPYANRE 408
Db 317 IMYELATHDPVQKLOEIDAVLPNKAPPTDYTLQMEYLDVMVNETLRLPFIAMLERV 376
Qy 409 CLKDEDFIPLAEPVIGRDSGVINEVRITKGTWYMLPLFNINRSKFIYGEDAEPPERLW 468
Db 377 CKKQVE-----INGMEIPKGVVVMIPSYALHRDP-KYWTEPEKFLPERFS 420
Qy 469 EDVTDLSNS-IEAPYGHQASFISSGRACFGRFAVAEMKAFIPLVTLRRVQFE 520
Db 421 KKNKDNIDPIYITPFG-----SGPRNCIGMRPALMMKALIRVLQNFSPFK 467
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; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7091
; LENGTH: 507
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-7091

Query Match      13.5%; Score 385; DB 2; Length 507;
Best Local Similarity 28.1%; Pred. No. 1.6e-29;
Matches 151; Conservative 84; Mismatches 196; Indels 106; Gaps 25;

Qy 13 LAAFSW--ASIAFSLYL-APRRSLYNLQ-PNHTNY-FTGNFLDILSARTG-----E 61
Db ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
12 LAVETWLLAVSLVLLYLGTRHGLFKRLGIPGPTPLPLLN---VLSYRQGLWKFDTE 68
Qy 62 BHAKYREKYGSTLRFAGIAGAPVLNSTDPKVPNHVM-KEAYDYPKPGWAARVLIATG-- 118
Db ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
69 CYKYGKQWGT---YEG--QLPVLAITDPDVRTVLVKECY-----SVFTNRRSLGPV 116
Qy 119 ----DGVVTAEGEAHRRHRIIMPISLAQAVKSMVPIFEKGMELVDKRMEDAAEKOMAV 174
Db ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
117 GFMSKSAISLAEDDEWKRIIRLSLPTFTSGKLKEMPPIIAQYGDVLRNLRE-AEKG--- 172
Qy 175 GESAGEKKATRLTEGVDKQWVGVRATLDVMAAGFDYKSDSLQ-----KTNELYVAF 228
Db ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
173 -----KPVTLKIDFGAYSMDVITGTSFGVNIIDSLNPNQDPFVVESTKKFLKF 218
Qy 229 VGLTDGFAPTLDSFKAIMWDFVPYFRTMKRHEIPLTQGLAVS--RRVGIELMEQKKQAV 286
Db ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
219 -----GFLDPL--FLSIIILFPEL-----TPVFALNVSLPPKOTINFLSKS----- 257
Qy 287 LGSASDAQVKKDQVGRDILSLVRANIAANLPESQKLSDBEVLAQISNLLFAGYETSST 346
Db ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
258 VNRMKSLRNDQKQRLDFQLMIDSONSKETESHKALSDELAQAQSIIFIFAGYETSS 317
Qy 347 VLTWMFHLRSEDKAVQDKLREICQI--DTDMPTLDELNALPYLEAFVKESLRDPPSPY 404
Db ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
318 VLSFTLYELATHPDVQKQLOKEIDAVLPNKAPPYDYAVVQMEYLDVMVNETLRLFPVAIR 377
Qy 405 ANRECLKDDEDFIPLAEPVIGRDSVINEVRITKGTMMVLPFNINRSKPIYGEDAERFP 464
Db ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
378 LERTCKKQVE-----INGVFIPKGSWVPIYALHHPD-KYWTEPEERFP 421
Qy 465 ERWLEDVDTSLNS-IEAPYGHQASISGPRACFGWRFAVAEMKAFPLVTLRRVQPEP 520
Db ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
422 ERFSKK-KDSIDPIYTFPG-----TGPRNCIGNRFPALMNMKLALIRVLQNFSPK 471
```

## RESULT 9

```
US-08-457-274A-25
; Sequence 25, Application US/08457274A
; Patent No. 5734086
; GENERAL INFORMATION:
; APPLICANT: Scott, Jeffrey G.
; APPLICANT: Tomita, Takashi
; TITLE OF INVENTION: Cytochrome P4501pr Gene and Its Uses
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle
; STREET: P.O. Box 1051, Clinton Square
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14603
```

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/457,274A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldman, Michael L.
; REGISTRATION NUMBER: 30,727
; REFERENCE/DOCKET NUMBER: 19603/240 (D-1519)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 716-263-1304
; TELEFAX: 716-263-1600
```

```
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 504 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Rat
; STRAIN:
; DEVELOPMENTAL STAGE: Adult
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; US-08-457-274A-25
```

```
Query Match      13.0%; Score 370; DB 1; Length 504;
Best Local Similarity 26.2%; Pred. No. 5e-28;
Matches 147; Conservative 84; Mismatches 189; Indels 140; Gaps 23;

Qy 7 LTGALGAASFASWASIAFFSLY-LAPRESSLVNLQ-----PNHTNYFTGNF-LDI 54
Db ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
3 LLSALTLETWLLAVLVLLYGFGRTHGLFKKQIGPQKPLPFGTIVLYMGLWKFDV 62
Qy 55 LSARTGBEHAKYREKYGSTLRFAGIAGAPVLNSTDPKVPNHVM-KEAY-----DYPKP 106
Db ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
63 -----ECHKYKGKING--LFQD--QMPLFAITDTEMIKNVLVKECFSVETNRDRFGPV 111
Qy 107 GMAARVLIATGQGVVTAEGEAHRRHRIIMPISLAQAVKSMVPIFEKGMELVDKXMD 166
Db ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
112 GI-----MGKAVSVAKDEWKRYRALLSPFTTSGLRKEMFPPII BOYGDI LVKYKQ 163
Qy 167 AAEKDMAVGESAGEKKATRLTET-EGVDVKQWVGVRATLDVMAAGFDYKSDSLQ----- 219
Db ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
164 A-----ETGKPVTKMKYFGAYSHDVITSTSGVNVDSLNPKDPFV 204
Qy 220 -KTNEL-----YVAFVGLTDGFAPTLDSFKAIMW--DFVPYFRTMKRHEIPL 264
Db ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
205 ETKTKLLRFDFPDLFLSVLFPFLT---PIYEMLNICMFPKDSIEPEK----- 250
Qy 265 TQGLAVSRVIGIELMEQKQAVLGSASDAQVKKDQVGRDILSLVRANIAANLPESQ-K 323
Db ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
251 -----KFYRMKTRLDSVQKRV-----DFLQLMNAHNSDKKESHTA 290
Qy 324 LSDREVLQAISNLLFAGYETSSTVLTWMFHLRSEDKAVQDKLREICQI--DTDMPTLDE 381
Db ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
291 LSDMEITHAQSIIFIFAGYEPTSSLSFVLHSLATHPTQKKLQBEIDRALPNKAPPTYDT 350
Qy 382 LNALPYLEAFVKESLRDPPSPYANRECLKDDEDFIPLAEPVIGRDSVINEVRITKGTW 441
Db ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
351 VMEMEYLDVMVNETLRLYPIGNRLERLVCKQVE-----INGVFMKPGSVV 395
Qy 442 MLPLFNINRSKPIYGEDAERFPERWLEDVDTSLNS-IEAPYGHQASISGPRACFGWR 500
Db ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
396 MIPSVALHRDPQHWPE-PEEFPRPFBSKENKGSIDPYVYLPFG-----NGPRNCIGMR 448
```

QY 501 AVAEMKAFVLTLLRRVQFEP 520  
 Db 449 ALMMKALTKVLQNFSPQ 468

RESULT 10  
 PCT-US95-05758-25  
 ; Sequence 25, Application PC/TUS9505758  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cornell Research Foundation, Inc.  
 ; TITLE OF INVENTION: Cytochrome P4501pr Gene and Its  
 ; NUMBER OF SEQUENCES: 29  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Nixon, Hargrave, Devans & Doyle  
 ; STREET: P.O. Box 1051, Clinton Square  
 ; CITY: Rochester  
 ; STATE: New York  
 ; COUNTRY: USA  
 ; ZIP: 14603  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/US95/05758  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Goldman, Michael L.  
 ; REGISTRATION NUMBER: 30,727  
 ; REFERENCE/DOCKET NUMBER: 19603/241 (D-1519)  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 716-263-1304  
 ; TELEFAX: 716-263-1600  
 ; INFORMATION FOR SEQ ID NO: 25:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 504 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; HYPOTHEICAL: NO  
 ; ANTI-SENSE: NO  
 ; ORIGINAL SOURCE:  
 ; ORGANISM: Rat  
 ; STRAIN: Unknown  
 ; DEVELOPMENTAL STAGE: Adult  
 ; POSITION IN GENOME:  
 ; CHROMOSOME/SEGMENT: Unknown  
 PCT-US95-05758-25

Query Match 13.0%; Score 370; DB 4; Length 504;  
 Best Local Similarity 26.2%; Pred. No. 5e-28;  
 Matches 147; Conservative 84; Mismatches 189; Indels 140; Gaps 23;

QY 7 LTGALGLAAFSWASIAFFSLY-LAPRRSSLYNLOG-----PNHTNYFTGNF-LDI 54  
 Db 3 LLSALTLETWLVAVLVLLYGTRTHGLPKQIGPGPLPFFGTVLNLYMGLWKFVD 62

QY 55 LSARTGEEHAKYREKYGSTLRPAGIAGAPVLNSTDPKVFNVHM-KEAY-----DYPKP 106  
 Db 63 -----ECHKYKGIWG---LFDG--QMPLFAITDTEMIKNVLVKCFSPVFNRRDFGPV 111

QY 107 GMAARVLRIATGCVVTAEGEAHKBHRRIMIPSLSAQAVKSVPIPLEKGMELVDKMD 166  
 Db 112 GI-----MGKAVSVAKDEEKWRALLSPFTTSGRLKEMFPPIIEQYGDILVLYLKO 163

QY 167 AAEKDMVAGESAGEKKATRLLET-EGVDVKDWGRATLDVNMALAGFDYKSDSLQN----- 219  
 Db 164 A-----ETGKPVTKKVFVAYSMDVITSTSGVNVDSLNNPKDPFV 204

QY 220 -KTNEL-----YVAFVGLTDGPAPTLDSFKAIMW--DFVPYFRTMKRRHEIPL 264  
 Db 205 ETKKLLRDFDFDLFLSVVLPFLT-----PIYEMLNICMFPKDSIEFFK----- 250

QY 265 TQGLAVSRRVGIEMEQKQAVLGSASDAQVDKQVQGRDILSLLYRANIAANLPSQ-K 323  
 Db 251 -----KFVTRMKETRLDSVQKHV-----DFLQMMNAHNDKDKESHYA 290

QY 324 LSDEEVLQAISNLLFAGYETSTVLTMFHRHSEDKAVQDKLREEICQI--DTDMPITLDE 381  
 Db 291 LSDMEITAQSIIFIFAGYEPTSTLSFVLHSLATHPTQKQLQEEIDRALPNKAPTYDT 350

QY 382 LNALPYLEAFVKESIRLDPPSPYANRECLKDEDFIPLAEPVIGRDSVINEVRIITGTMV 441  
 Db 351 VMEMEYLDVNLNETRLYPIGNRLRVERVCKDVE-----INGVFMPKGSVV 395

QY 442 MLPLFNINRSKFTYGEDAEFEFRPERWLEDVDTSLNS-IEAPYGHQASFISGPRACFGWRF 500  
 Db 396 MIPSYALHRDPQHWPE-PHEFRPERFSKENKSIDPYVLPFG-----NGPRNCIGMRF 448

QY 501 AVAEMKAFVLTLLRRVQFEP 520  
 Db 449 ALMMKALTKVLQNFSPQ 468

RESULT 11  
 US-09-527-073-2  
 ; Sequence 2, Application US/09527073  
 ; Patent No. 6534313  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Michael M. Neff  
 ; APPLICANT: Joanne Chory  
 ; TITLE OF INVENTION: GENETICALLY MODIFIED PLANTS HAVING  
 ; TITLE OF INVENTION: MODULATED BRASSINOSTEROID SIGNALING  
 ; FILE REFERENCE: SALKINS.024A  
 ; CURRENT APPLICATION NUMBER: US/09/527,073  
 ; CURRENT FILING DATE: 2000-03-16  
 ; PRIOR APPLICATION NUMBER: US 60/124570  
 ; PRIOR FILING DATE: 1999-03-16  
 ; PRIOR APPLICATION NUMBER: US 60/170,931  
 ; PRIOR FILING DATE: 1999-12-14  
 ; PRIOR APPLICATION NUMBER: US 60/172,832  
 ; PRIOR FILING DATE: 1999-12-20  
 ; NUMBER OF SEQ ID NOS: 16  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 2  
 ; LENGTH: 520  
 ; TYPE: PRT  
 ; ORGANISM: Arabidopsis thaliana  
 US-09-527-073-2

Query Match 12.9%; Score 367; DB 2; Length 520;  
 Best Local Similarity 22.2%; Pred. No. 1.1e-27;  
 Matches 128; Conservative 111; Mismatches 203; Indels 134; Gaps 21;

QY 4 LVLLTGALGLAAFSWASIAFFSLYLAAPRR-----SSLNLOGNHTNYFTGNFLDILS--- 56  
 Db 13 VLVLVSILSLVIVKMSL-----LWWRPKIEHFSKQIGRGPY-HFFIGNVKELVGMML 67

QY 57 -----ARTGEEHAKYREKYGSTLRPAGIAGAPVLNST--DPKVFNVHMKEA 100  
 Db 68 KASSHPMPFSSHNLPRVLSFVHHWRKIYGATFL---VWFGPTFRLTVADPDILREIFS 124

QY 101 YDYPKPGWAARVLRIATGCVVTAEGEAHKBHRRIMIPSLSAQAVKSVPIPLEKGMELV 160  
 Db 125 EFYER-NEAHPVLKQLEGDGLLSLKGEKWAHHRKIISPTFMENLKLIVPVVLKSVTDM 183

QY 161 DKWMDAAEKDMVAGESAGEKKATRLLETGVDVKDWGRATLDVNMALAGFDYKSDSLQN 220  
 Db 184 DKWSDKLSN-----GEVE-----VDVWEMFQILTEDVISRTAFGSSYE----- 222

QY 221 TNELYVAFVGLTDGPA-----TLDSFKAIMWDFVPYFRTMKRRHEIPLTQGLAV 270



1	PRIOR APPLICATION NUMBER: 60/089600
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3	PRIOR APPLICATION NUMBER: 60/089653
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5	PRIOR APPLICATION NUMBER: 60/089801
6	PRIOR FILING DATE: 1998-06-18
7	PRIOR APPLICATION NUMBER: 60/089907
8	PRIOR FILING DATE: 1998-06-18
9	PRIOR APPLICATION NUMBER: 60/089908
10	PRIOR FILING DATE: 1998-06-18
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14	PRIOR FILING DATE: 1998-06-19
15	PRIOR APPLICATION NUMBER: 60/089952
16	PRIOR FILING DATE: 1998-06-19
17	PRIOR APPLICATION NUMBER: 60/090246
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19	PRIOR APPLICATION NUMBER: 60/090252
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63	PRIOR APPLICATION NUMBER: 60/091360
64	PRIOR FILING DATE: 1998-07-01
65	PRIOR APPLICATION NUMBER: 60/091478
66	PRIOR FILING DATE: 1998-07-02
67	PRIOR APPLICATION NUMBER: 60/091544
68	PRIOR FILING DATE: 1998-07-01
69	PRIOR APPLICATION NUMBER: 60/091519
70	PRIOR FILING DATE: 1998-07-02
71	PRIOR APPLICATION NUMBER: 60/091626
72	PRIOR FILING DATE: 1998-07-02
73	PRIOR APPLICATION NUMBER: 60/091633

; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09
;
Query Match 12.1%; Score 346.5; DB 2; Length 524;
Best Local Similarity 23.6%; Pred. No. 1.2e-25;
Matches 140; Conservative 104; Mismatches 211; Indels 137; Gaps 26;
Qy 3 ILVLTGALGIA-AFSWASIAFFSLYLAPRSSLYNLQGNHTYFTGNFLDILSARTG- 60
Db 21 LLLVWGSWLLARILAWT---YAFYNNCR--LQCFPPQPKRWFWGHLGLIPTTEGL 74
Qy 61 ---EEHAKYREKYGSTLRPAGIAGAPVLNSTDPKFNHVMK-BAYDYPKPGMAARVLR 115
Db 75 KDSQMSATYSQ--GFTVWLGPI--IPFVILCHDPTIRSIITNAAAPKDNLFIRFLKP 130
Qy 116 ATGDGVVTAEGEAKHRRRIMIPSLAQAVKSMVPIFEKGMELVDKMDAEDAKOMAVG 175
Db 131 WLGEILLSGGDKWSRRRMLTPAFHFENILKSYITFNKSNIMLDKWQLHASE-----G 185
Qy 176 ESAGEKKAIRLETGVVDKDWGRATLDVMALAGFDYKSDSLQNKWELVYVAVGLTDFG 235
Db 186 SSR-----LDMFEHISLMTLDSLQKCFSDS-HCQBRPSE-YIA----- 223
Qy 236 APTLDSFKAIM-----WDFVPYFR-----TWKRRHEIPLT 265
Db 224 ---TILELSALVEKRSQHILQHMDFLYLSDGRFHRACRLVHDFDAVIRERTLP-T 280
Qy 266 QGLAVSRVGIELMEQKQAVIGSASQAVDKDVQGRDILSLVRAIANALPESOKLS 325
Db 281 QGI-----DDFFKOKAKSKTLDLFDVL-----LLSKDGDGKALS 314
Qy 326 DEEVLAQISNLLFAGYETSSVLTWMFRLSEDKAVQDKLEEICQI---DMDMTL--DE 381
Db 315 DEDIRAEADTTFMGHGDHTASGLSVLYNLARHPEYQERCRQEOELLKDRDPKEIEWDD 374
Qy 382 LNALPYLEAFVKESLRDPPSPYANRECLKDEDPIPLAEPVIGRDSVINEVRIKGMV 441
Db 375 LAQLPFLTWCVESLRLLHPAPFISRCTQD-----IVLPDGRV-----IPKGITC 420
Qy 442 MLPLFNINRSFIYGEDAEFRPERWLEDVTDLSLSI-EAPYGHQAQFISGPRACFGWRF 500
Db 421 LIDIIGVHHNPTVM-PDPEVYDPPRF-----DPENSKGRSPLAF-IPFSAGFRNCIGQAF 473
Qy 501 AVAEMKAFVTLRRVQFEPIISHPEYEHITLIISRPRIVGREKEGYQMRLO 552
Db 474 AMAEMKVVLMLLHFLRFLPDHTEPR-----RKLELIMRAEGGLWLRVE 517
;
RESULT 14
US-09-990-444-264
; Sequence 264, Application US/09990444
; Patent No. 6930170
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
;
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas P.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
;
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC19
; CURRENT APPLICATION NUMBER: US/09/990,444
; CURRENT FILING DATE: 2001-11-14
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; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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;	PRIOR FILING DATE: 1998-07-09	

Query Match	12.1%	Score 346.5;	DB 2;	Length 524;
Best Local Similarity	23.6%	Pred. No. 1.2e-25;		
Matches 140;	Conservative 104;	Mismatches 211;	Indels 137;	Gaps 26;

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Query Match 12.1%; Score 346.5; DB 2; Length 524;  
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Matches 140; Conservative 104; Mismatches 211; Indels 137; Gaps 26;  
QY 3 ILVLLTGALGA-AFWSASTAFSLYLAPERSLYNLOGPNHTNYFTGNFLDILSARTG- 60  
Db 21 LLLLVGWSLLARILAWT-----YAFYNNCR--LQCFPPQPKRNFWFGLITPTEGL 74

QY 61 -----EEHAKYREKYGSTLRFAGIAGAPVLNSTDPKVENHVMK-EAYDYKPKGMAARVLR1 115  
Db 75 KDSTQMSATYSQ--GFTVWLGP1--IPFIVLCHPDTRISITWASAAIAIPKONLFIKLP 130  
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QY 176 ESAGEKKATRLTEGVDVVDWGRATLDVMALAGPDYKSDSLQNKTNELYVAFVGLTDGF 235  
Db 186 SSR-----LDMEHISLMTLDSLKQCFSDS-HCQRPSE-YIA----- 223  
QY 236 APTLDSFKAIM-----WDFVPYFR-----TMKRRHEIPT 265  
Db 224 --TILELSALVEKRSQHILQHMDFLYYLGHGRRFHRACRLVHDTTDAVIRRRRTLP-T 280  
QY 266 QGLAVSRRVGIELMEQKQAVLGSASDOAVDKKQVQGRDILSLVPRANTAANLPESOKLS 325  
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Db 315 DEDIRAEADTFMGGHDTTASGLSWLYNLAHPEYQECRCQEVQELLKDRDPKLEWDD 374  
QY 382 LNALPYLEAFVYESLRDPPSPYANRECLKDEDFIPLAEPVIGRSGSVINEVRITKGMV 441  
Db 375 LAQLPFLTMCVKESLRLLHPPAPFISRCTQD-----IVLPDGRV-----IPKGITC 420  
QY 442 MLPLFNINRSKFTYGEDAEERPERWLEDVTDLSNSI-EAPYGHQASFTSGPRACFGWRF 500  
Db 421 LIDIIGVHNPTVW-PDPEVDPFRF-----DPENSKGRSPLAF-IPFSAGPRNCIGQAF 473  
QY 501 AVAEMKAFLEVTLRVQFEPFIISHPEYEHITLIISPRIVGREKEGYQMRLQ 552  
Db 474 AMAENKVVLALMLLHFRFLPDHTEPR-----RKLEIMRAEGLWLRLVE 517

Search completed: November 21, 2005, 16:57:08  
Job time : 29 secs